

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2005, 08:58:09 ; Search time 232 Seconds
(without alignments)

1222.510 Million cell updates/sec

Title: US-10-506-406-2

Perfect score: 2071
Sequence: 1 MQMSPALTCVLGLALVFE.....FVVRHNPCTGVLFGQWNEP 402

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2071	100.0	402	PA11_HUMAN	P05121 homo sapien
2	2019	97.5	402	Q8WND4_CERAE	Q8WND4 cercopithec
3	1790	86.4	402	PA11_PIG	P79335 sus scrofa
4	1784	86.1	402	PA11_BOVIN	P13909 bos taurus
5	1746	84.3	400	PA11_MUSVI	P50449 mustela vis
6	1680	81.1	402	PA11_RAT	P20961 rattus norv
7	1631	78.8	402	Q7TPP9_MOUSE	Q7TPP9 mus musculu
8	1626	78.5	402	PA11_MOUSE	P22777 mus musculu
9	1256	60.6	280	Q8MI31_HORSE	Q8MI31 equus cabal
10	863	41.7	182	Q77772_RABIT	Q77772 oryctolagus
11	842	40.7	395	Q6DD81_XENLA	Q6DD81 xenopus lae
12	796.5	38.5	397	1 GDN_MOUSE	Q07235 mus musculu
13	796.5	38.5	397	Q543R5_MOUSE	Q543R5 m 16 days e
14	796.5	38.5	397	Q4FJUI_MOUSE	Q4FJUI mus musculu
15	791.5	38.2	397	1 GDN_RAT	P07092 rattus norv
16	781.5	37.7	397	Q8HZY1_BOVIN	Q8HZY1 bos taurus
17	779.5	37.6	397	Q8WNW8_PIG	Q8WNW8 sus scrofa
18	770.5	37.2	397	Q5D0C4_HUMAN	Q5D0C4 homo sapien
19	761	36.7	397	Q4RYZ2_TETNG	Q4RYZ2 tetraodon n
20	761	36.7	398	1 GDN_HUMAN	P07093 homo sapien
21	761	36.7	398	Q53815_HUMAN	Q53815 homo sapien
22	756.5	36.5	395	Q7ZVL5_BRARE	Q7ZVL5 brachydanio
23	721.5	34.8	330	Q4TBF0_TETNG	Q4TBF0 tetraodon n
24	620	29.9	410	1 NEUS_CHICK	Q09035 gallus gall
25	609	29.4	410	Q6GLT7_XENLA	Q6GLT7 xenopus lae
26	604	29.2	410	1 NEUS_RAT	Q9J1D2 rattus norv
27	594	28.7	410	1 NEUS_MOUSE	Q35684 mus musculu
28	594	28.7	410	Q543F7_MOUSE	Q543F7 m 12 days e
29	593	28.6	410	1 NEUS_HUMAN	Q99574 homo sapien
30	593	28.6	410	Q6AHZ4_HUMAN	Q6AHZ4 homo sapien
31	588	28.4	383	Q9DHV2_YLDV	Q9DHV2 yaba-like d

Q6P808 xenopus tro
Q5U527 xenopus lae
Q6HA07 branchioeto
Q5FVZ7 xenopus tro
Q64HW4 oncorhynchu
Q75830 homo sapien
Q7YSA1 canis famli
Q8BH11 mus musculu
Q6UKZ2 mus musculu
Q9DIQ5 mus musculu
Q6R745 canis famli
Q8TGUL brachydanio
P80229 sus scrofa
Q9JK88 mus musculu

32 569.5 27.5 315 2 Q6P808_XENTR
33 564 27.2 433 2 Q5U527_XENLA
34 554.5 26.8 407 2 Q6HA07_BRALA
35 548.5 26.5 410 2 Q5FVZ7_XENTR
36 546.5 26.4 380 2 Q64HW4_ONCHY
37 534 25.8 405 1 SPI2_HUMAN
38 529 25.5 125 2 Q7YSA1_CANFA
39 525 25.4 387 2 Q8BH11_MOUSE
40 524 25.3 387 2 Q6UKZ2_MOUSE
41 523 25.3 387 2 Q9DIQ5_MOUSE
42 519 25.1 123 2 Q6R745_CANFA
43 513.5 24.8 384 2 Q6TGUL_BRARE
44 511.5 24.7 378 1 ILEU_PIG
45 510 24.6 405 1 SPI2_MOUSE

ALIGNMENTS

RESULT 1

PA11_HUMAN
ID PA11_HUMAN STANDARD; PRT; 402 AA.
AC P05121;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial
DE plasminogen activator inhibitor) (PAI).
GN Name=SERPINE1; Synonym=PAI1, PLANH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87053819; PubMed=2430793;
RA Pannecoek H., Veerman H., Lambers H., Diergaarde P., Verweij C.L.,
RA van Zonneveld A.-J., van Mourik J.A.;
RT "Endothelial plasminogen activator inhibitor (PAI): a new member of
the Serpin gene family.";
RL EMBO J. 5:2539-2544 (1986).
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=89000586; PubMed=2820474;
RA Loskutoff D.J., Linders M., Keijer J., Veerman H.,
RA van Heerikhuizen H., Pannecoek H.;
RT "Structure of the human plasminogen activator inhibitor 1 gene:
nonrandom distribution of introns.";
RL Biochemistry 26:3763-3768 (1987).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=87058123; PubMed=3097076;
RX Ginsburg D., Zehab R., Yang A.Y., Rafferty U.M., Andreasen P.A.,
RA Nielsen L., Dano K., Lebo R.V., Gelehrter T.D.;
RT "cDNA cloning of human plasminogen activator-inhibitor from
endothelial cells.";
RL J. Clin. Invest. 78:1673-1680 (1986).
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=90128289; PubMed=2612914; DOI=10.1016/0378-1119(89)90519-2;
RA Folio M., Ginsburg D.;
RT "Structure and expression of the human gene encoding plasminogen
activator inhibitor, PAI-1.";
RL Gene 84:447-453 (1989).
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=89005111; PubMed=3262512;
RA Strandberg L., Lawrence D., Ny T.;
RT "The organization of the human-plasminogen-activator-inhibitor-1 gene.
RT implications on the evolution of the serine-protease inhibitor
family.";
RL Eur. J. Biochem. 176:609-616 (1988).

- [6] NUCLEOTIDE SEQUENCE.
 RP MEDLINE=88243790; PubMed=3132455;
 RA Bosma P.J., van den Berg E.A., Kooistra T., Siemieniak D.R.,
 RA Slightom J.L.;
 RT "Human plasminogen activator inhibitor-1 gene. Promoter and structural
 gene nucleotide sequences";
 RL J. Biol. Chem. 263:9129-9141(1988).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Pannekoeck H.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 [8]
 RP INTERACTION WITH VTN.
 RX MEDLINE=94368811; PubMed=7522053; DOI=10.1016/0167-4838(94)90166-X;
 RA Sigurdardottir O., Wiman B.;
 RT "Identification of a PAI-1 binding site in vitronectin.";
 RL Biochim. Biophys. Acta 1208:104-110(1994).
 [9]
 RP NUCLEOTIDE SEQUENCE.
 RA Cordes M., Doela D.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 [10]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS THR-15; ILE-17;
 PRO-25; HIS-209 AND ASN-255.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-
 FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [11]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J.J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Beasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [12]
 RP NUCLEOTIDE SEQUENCE OF 20-402.
 RX MEDLINE=86313660; PubMed=3092219;
 RA Ny T., Sawdey M., Lawrence D., Millan J.L., Loskutoff D.J.;
 RT "Cloning and sequence of a cDNA coding for the human beta-migrating
 endothelial-cell-type plasminogen activator inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6776-6780(1986).
 [13]
 RP NUCLEOTIDE SEQUENCE OF 1-47 AND 364-402.
 RX MEDLINE=87080762; PubMed=3025016; DOI=10.1016/0014-5793(86)81113-9;
 RA Andreason P.A., Riccio A., Welinder K.G., Douglas R., Sartorio R.,
 RA Nielsen L.S., Oppenheimer C., Blasi F., Danoe K.;
 RT "Plasminogen activator inhibitor type-1: reactive center and amino-
 terminal heterogeneity determined by protein and cDNA sequencing.";
 RL FEBS Lett. 209:213-218(1986).
 [14]
 RP NUCLEOTIDE SEQUENCE OF 17-402, AND PARTIAL PROTEIN SEQUENCE.
 RP TISSUE=Placenta;
 RX MEDLINE=87105925; PubMed=3026837; DOI=10.1016/0014-5793(87)81288-7;
 RA Mun T.C., Kretzmer K.K.;
 RT "cDNA cloning and expression in E. coli of a plasminogen activator
 inhibitor (PAI) related to a PAI produced by Hep G2 hepatoma cell.";
 RL FEBS Lett. 210:11-16(1987).
 [15]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=92114970; PubMed=1731226; DOI=10.1038/355270a0;
 RA Mottonen J., Strand A., Symersky J., Sweet R.M., Danley D.E.,
 RA Geoghegan K.F., Gerard R.D., Goldsmith E.J.;
 RT "Structural basis of latency in plasminogen activator inhibitor-1.";
 RL Nature 355:270-273(1992).
 [16]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96003732; PubMed=7552714;
 RA Aertgeerts K., de Bondt H.L., de Ranter C.J., Declerck P.J.;
 RT "Mechanisms contributing to the conformational and functional
 flexibility of plasminogen activator inhibitor-1.";
 RL Nat. Struct. Biol. 2:891-897(1995).
 [17]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE=98298439; PubMed=9634700; DOI=10.1016/S0969-2126(98)00064-1;
 RA Xue Y., Bjoerquist P., Inghardt T., Linschoten M., Musil D.,
 RA Sjoelin L., Deinum J.;
 RT "Interfering with the inhibitory mechanism of serpins: crystal
 structure of a complex formed between cleaved plasminogen activator
 inhibitor type 1 and a reactive-centre loop peptide.";
 RL Structure 6:627-636(1998).
 [18]
 RP X-RAY CRYSTALLOGRAPHY (2.99 ANGSTROMS).
 RX MEDLINE=99148119; PubMed=10368279; DOI=10.1016/S0969-2126(99)80018-5;
 RA Sharp A.M., Stein P.E., Pannu N.S., Carrell R.W., Berkenpas M.B.,
 RA Ginsburg D., Lawrence D.A., Read R.J.;
 RT "The active conformation of plasminogen activator inhibitor 1, a
 target for drugs to control fibrinolysis and cell adhesion.";
 RL Structure 7:111-118(1999).
 [19]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=20198318; PubMed=10731421; DOI=10.1006/jmbi.2000.3604;
 RA Nar H., Bauer M., Staessen J.M., Lang D., Gils A., Declerck P.J.;
 RT "Plasminogen activator inhibitor 1. Structure of the native serpin,
 comparison to its other conformers and implications for serpin
 inactivation.";
 RL J. Mol. Biol. 297:683-695(2000).
 [20]
 RP VARIANT THR-15.
 RX MEDLINE=97337920; PubMed=9194591;
 RA Turkmen B., Schmitt M., Schmalfeldt B., Trommler P., Hell W.,
 RA Creutzburg S., Graeff H., Magdolen V.;
 RT "Mutational analysis of the genes encoding urokinase-type plasminogen
 activator (uPA) and its inhibitor PAI-1 in advanced ovarian cancer.";
 RL Electrophoresis 18:686-689(1997).
 [21]
 RP VARIANTS THR-15 AND ILE-17.
 RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 of human genes";
 RL Nat. Genet. 22:231-238(1999).
 [22]
 RP ERRATUM.
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373(1999).
 [23]
 RP INTERACTION WITH LRP1B.
 RX MEDLINE=21369943; PubMed=11384978; DOI=10.1074/jbc.M102727200;
 RA Liu C.-X., Li Y., Obermoeller-McCormick L.M., Schwartz A.L., Bu G.;
 RT "The putative tumor suppressor LRP1B, a novel member of the low

QY 1 MQMSPALTCILVLGLALVFGESAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSFY 60

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DR SMR; P79335; 26-402.
DR InterPro; IPR000215; Prot_inh_serpin.
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Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DR PFam: PF00079: Serpin; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Glycoprotein; Plasma; Plasminogen activation; Protease inhibitor;
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 402 Plasminogen activator inhibitor-1.
FT SITE 369 370 Reactive bond.
FT CARBOHYD 232 232 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 288 288 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 352 352 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 402 AA; 45450 MW; 13F60E5F4F8FE405 CRC64;

Query Match 86.4%; Score 1790; DB 1; Length 402;
Best Local Similarity 86.3%; Pred. No. 1.9e-135;
Matches 34; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQSKDRNVFSPY 60
Db 1 MRMSLVFACLAMGLALTFAEGSSASHQSLAARLATDFGVKVFQVQVQASKDRNVFSPY 60

Qy 61 GVASVLAMQLTTCGETQQOIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTCAGTQQOIQEAMQFKIEKGMAPALRQLYKELMGPNKDEISTADAI 120

Qy 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVTKHKGMSNLLGKGAV 180
Db 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEMDRARFIINDWVKRTHKGMSNLLGOGAV 180

Qy 181 DQLTRVLVNLALYFNGQWKTFFPDSTHRLRFHKSOGSTSVSPVMAQTNKFNTFTPTD 240
Db 181 DQLTRVLVNLALYFNGQWKTFFPEKSTHRLRFHKSOGSTSVSPVMAQTNKFNTFTPTD 240

Qy 241 GHYYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSQAQLSHWKGNTRLRLVLPK 300
Db 241 GHYYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSQAQLSHWKGNTRLRLVLPK 300

Qy 301 FSLTEVDLRKPLENLGMDTMRFOQADFTSLSDQEPHVAQALQKVIENESGTVASS 360
Db 301 FSLSEVDLRKPLENLGMDTMRFNQADFTSLSDQELLYMSQALQKVIENESGTVASS 360

Qy 361 STAVIVSARMAPEIIMDRPFLFVVRHNPVTGLVFMGQVMEP 402
Db 361 STAIIVSARMAPEIIMDRPFLFVVRHNPVTGLVFMGQVMEP 402

RESULT 4
PAIL BOVIN STANDARD; PRT; 402 AA.
AC P13909;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial
DE plasminogen activator inhibitor) (PAI).
GN Name=SERPINE1; Synonyms=PAI1;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9006786; PubMed=2587231;
RA Mamuro J., Sawday M., Hattori M., Loskutoff D.J.;
RT "cDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).";
RL Nucleic Acids Res. 17:8872-8872(1989).
RN [2]
RP PROTEIN SEQUENCE OF 24-63.
RX MEDLINE=88329072; PubMed=3262060;
RA Katagiri K., Okada K., Hattori H., Yano M.;
RT "Bovine endothelial cell plasminogen activator inhibitor. Purification
RT and heat activation.";
RL Eur. J. Biochem. 176:81-87(1988).

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RN RP NUCLEOTIDE SEQUENCE OF 153-235.
RX TISSUE=Adrenal cortex;
RC MEDLINE=90338128; PubMed=1696269; DOI=10.1083/jcb.111.2.743;
RA Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
RT "Transforming growth factor-beta 1 modulates basic fibroblast growth
RT factor-induced proteolytic and angiogenic properties of endothelial
RT cells in vitro.";
RL J. Cell Biol. 111:743-755(1990).
CC -1- FUNCTION: This inhibitor acts as "bait" for tissue plasminogen
CC activator, urokinase, and protein C. Its rapid interaction with
CC tPA may function as a major control point in the regulation of
CC fibrinolysis.
CC -1- SUBUNIT: Interacts with VTN. Binds LRP1B; binding is followed by
CC internalization and degradation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Vascular endothelial cells may be the primary
CC site of synthesis of plasma PAI.
CC -1- SIMILARITY: Belongs to the serpin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X16383; CAA34419.1; -; mRNA.
DR EMBL; X52906; CAA37094.1; -; mRNA.
DR PIR; S06745; S06745.
DR HSP; P05121; 9PAI.
DR SMR; P13909; 25-402.
DR InterPro; IPR000215; Prot_inh_serpin.
DR PANTHER; PTHR11461; Prot_Inh_serpin; 1.
DR Pfam; PF00079; Serpin; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Direct protein sequencing; Glycoprotein; Plasma;
KW Plasminogen activation; Protease inhibitor; Serine protease inhibitor;
KW Serpin; Signal.
FT CHAIN 1 23 Plasminogen activator inhibitor-1.
FT SITE 369 370 Reactive bond.
FT CARBOHYD 232 232 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 288 288 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 352 352 N-linked (GlcNAc... ) (Potential).
FT CONFLICT 50 50 S -> L (in Ref. 2).
SQ SEQUENCE 402 AA; 45371 MW; 905361733C7D130 CRC64;

Query Match 86.1%; Score 1784; DB 1; Length 402;
Best Local Similarity 85.3%; Pred. No. 5.9e-135;
Matches 34; Conservative 29; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQSKDRNVFSPY 60
Db 1 MRMSVPFACIALGALIFGEGSASYQPSAASLATDFGVKVFQVVRASKDRNVFSPY 60

Qy 61 GVASVLAMQLTTCGETQQOIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTCGETQQOIQEAMQFKIEKGMAPAFHRLYKELMGPNKDEISTADAI 120

Qy 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVTKHKGMSNLLGKGAV 180
Db 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVKRTHKGMSNLLGEGAV 180

Qy 181 DQLTRVLVNLALYFNGQWKTFFPDSTHRLRFHKSOGSTSVSPVMAQTNKFNTFTPTD 240
Db 181 DQLTRVLVNLALYFNGQWKTFFPESNTHRLRFHKSOGSTSVSPVMAQTNKFNTFTPTD 240

Qy 241 GHYYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSQAQLSHWKGNTRLRLVLPK 300
Db 241 GHYYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSQAQLSHWKGNTRLRLVLPK 300

Qy 301 FSLTEVDLRKPLENLGMDTMRFOQADFTSLSDQEPHVAQALQKVIENESGTVASS 360

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Db 301 FSLTEIDLRPLENIGMTDFRPSQADFSFSFSDQEFLYVSQALQKVKIEVNESGTLASS 360
Qy 361 STAVIVSARMAPEIINDRPFLFVVRNPTGTVLFMGQVMEP 402
Db 361 STALVVSARMAPEIINDRPFLFVVRNPTGTVLFMGQVMEP 402

RESULT 5
PAIR MUSVI
ID PAIR MUSVI STANDARD; PRT; 400 AA.
AC P50449;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial
DE plasminogen activator inhibitor (PAI).
GN Name=SERPINE1; Synonyms=PAI-1, PAI1, PLANH1;
OS Mus musculus (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Mustelidae;
OC Mustelinae; Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=96032362; PubMed=7557448; DOI=10.1016/0378-1119(95)00261-4;
RA Chuang T.H., Hamilton R.T., Nilsen-Hamilton M.;
RT "Cloning of the mink plasminogen activator inhibitor type-1 messenger
RT RNA: an mRNA with a short half life.";
RL Gene 162:303-308(1995).
CC -!- FUNCTION: This inhibitor acts as "bait" for tissue plasminogen
CC activator, urokinase, and protein C. Its rapid interaction with
CC TPA may function as a major control point in the regulation of
CC fibrinolysis.
CC -!- SUBUNIT: Interacts with VTN. Binds LRP1B; binding is followed by
CC internalization and degradation (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the serpin family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; X58541; CAA41433.1; -; mRNA.
PIR; JC4265; JC4265.
HSP; P05121; 9PAI.
SMR; P50449; 30-400.
DR InterPro; IPR000215; Prot_inh_serpin.
DR PANTHER; PTHR11461; Serpin; 1.
DR Pfam; PF00079; Serpin; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Glycoprotein; Plasma; Plasminogen activation; Protease inhibitor;
KW Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 400 Plasminogen activator inhibitor-1.
FT SITE 367 368 Reactive bond (By similarity).
FT CARBOHYD 230 230 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 286 286 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 350 350 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 400 AA; 45153 MW; DF45E0694DE28401 CRC64;

Query Match 84.3%; Score 1746; DB 1; Length 400;
Best Local Similarity 85.3%; Pred. No. 6.7e-132;
Matches 343; Conservative 25; Mismatches 32; Indels 2; Gaps 1;

Qy 1 MQNSPALTCVLGLALVFGEGSVAHHPPSVVAHLASDFGVRVFOQVAQSKDRNVVFSY 60
Db 1 MQMS--TVCLALGLALVFGESASYLHETRAELATDFGVKVFQVAQSKDRNVVFSY 58
Qy 61 GVASVLAMQLQTGGTQQIQAMGFKIDDGMAPALRHLYKELMGPNKDEISTDAI 120

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Qy 287 GNTRLRLPLVLPKFSLETEVDLRKPLENKGMDTDMFQFQADFTSLSDQEPFLHVAQALQK 346
Db 181 RSMTRVRLVLLPKFSLESEVDLRKPLENKGMDTDMFQFQADFTSLSDQEPFLHVAQALQK 240
Qy 347 VKIEVNSGTVASSSTAVIVSARMAPEEIIINDRPLFLVVR 386
Db 241 VKIEVNSGTVASSSTGTVSARMAPEEIIINDRPLFLVVR 280

RESULT 10

O77772_RABIT PRELIMINARY; PRT; 182 AA.
AC O77772;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Putative plasminogen activator inhibitor-1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Yin J., Idell S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AF074325; AAC62632.1; -, mRNA.
DR HSP; P05121; I1J5.
DR SMR; O77772; 1-182.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Serpin.
FT NON_TER 1 1
SQ NON_TER 182 182
SQ SEQUENCE 182 AA; 20920 MW; B2B6AEB6D92E217F CRC64;

Query Match 41.7%; Score 863; DB 2; Length 182;
Best Local Similarity 88.5%; Pred. No. 2.9e-61;
Matches 161; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 101 LYKELMGPNKDEISTTDAIFVQRDLKLVQGFMPHFLRSTVKQVDFSEVERARFIIN 160
Db 1 LSKELMGPNKDEISTTDAIFVQRDLKLVQGFMPHFLRSTVKQVDFSDVQARFIIN 60
Qy 161 DWVTKTKGMSNLLKGAVDQLTRLVLVNLALYFNGQWKTFFPSSTHRLFLFKSDGSTV 220
Db 61 DWVRHTKGMISDLLEGAMDQLTLVLVNLALYFNGQWKTFFPSKSGTHRVFKSDGSTI 120
Qy 221 SVPMMAQTNKFNTEFTPDGHYYDILELPVHGDTLSMFIAAPYEKSVPLSALTNILSAQ 280
Db 121 SVPMMAQTNKFNTEFTPDGHYYDILELPVHGDTLSMFIAAPYEKSVPLSALTNILSAQ 280
Qy 281 LI 282
Db 181 LI 182

RESULT 11

Q6DD81_XENLA PRELIMINARY; PRT; 395 AA.
ID Q6DD81_XENLA PRELIMINARY;
AC Q6DD81;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DB Serpine2-prov protein.
GN Name=serpine2-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN 2
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heigh F.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Spapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 3
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC077742; AAH7742.1; -, mRNA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 395 AA; 43985 MW; 7B0CD19F934AB1EE CRC64;
Query Match 40.7%; Score 842; DB 2; Length 395;
Best Local Similarity 45.0%; Pred. No. 4.1e-59;
Matches 170; Conservative 68; Mismatches 132; Indels 8; Gaps 4;
Qy 28 PSVAHIASDFGVRFVQVQAQAKDRNVSPYGVASVLAMQLTTCGETQQQIOAANGF 87
Db 23 PLSLEELGSDIGIQVFNQVARTPHENIVMSPHGISVLGLQGLGADGRTRKQLMTVMRY 82
Qy 88 KIDDKGMAPALRHLKELMGPNKDEISTTDAIFVQRDLKLVQGFMPHFLRSTVKQV 147
Db 83 KINE--VAKSLKTKNRAIVAKKQNDIVTANGVFASAFKVGFSVYKKNKDIHFSDVRSV 140
Qy 148 DFSEVERAREIINDWVKRTHTKGMSNLLKGAVD-QLTRLVLVNLALYFNGQWKTFFPDSS 206
Db 141 DFQEKNTAASIINQWVKQTKGMIEGLISPELDDSSVTRLVLVNLALYFKGLWKSRRHPEN 200
Qy 207 THRRLFKSDGSTSVSPMMAQTNKFNTEFTPDGHYYDILELPVHGDTLSMFIAAPYEK 266
Db 201 TKKRTFHGPDGKQVQVPMPLAQLSLFRSGSASTNGLWYNVIELPYHGGISMLVALPTEK 260
Qy 267 EVPLSALTNILSAQLISHWKGNTRIPR--LLVLPKFSLETEVDLRKPLENKGMDTDMFRQ 324

Db 261 STPLSALPHISTKLSW---MTMSPKRVOLLILPKFSVEAEADLKPSLNLGITMPDV 317
Qy 325 FQADFTSLSDQELHVAQAQKQKIVNESCTVASSSTAVIVSARMAPESIIIMDRPFLV 384
Db 318 SKANFAKISRESLHVSHLQAKIEVNECTKAGATTAVLIARSSPRWFTVDRPELFF 377
Qy 385 VRHNPPTGTVLPMQUMEP 402
Db 378 IHRNPTGAVLFTGQINKP 395

RESULT 12
GDN_MOUSE
ID GDN_MOUSE STANDARD; PRT; 397 AA.
AC Q07235; Q92117;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1) (Serine
protease-inhibitor-4).
GN Name=Serpine2; Synonyms=Pi7, Pnl, Spi4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Belin D.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1-366.
RC STRAIN=BALB/c;
RX MEDLINE=93259128; PubMed=8491179;
RA Vasealli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,
RA Velardi A., Wohlwend A., Erno H., Monard D., Belin D.;
RT "Protease-nexin I as an androgen-dependent secretory product of the
murine seminal vesicle.";
RL EMBO J. 12:1871-1898(1993).
CC -1- FUNCTION: Serine protease inhibitor with activity toward thrombin,
trypsin, and urokinase. Promotes neurite extension by inhibiting
thrombin. Binds heparin.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Most abundant in seminal vesicles.
CC -1- SIMILARITY: Belongs to the serpin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not

CC removed.
CC EMBL; X70296; CAA49777.1; -; mRNA.
DR EMBL; BC010675; AAH10675.1; -; mRNA.
DR EMBL; X70946; CAA50285.1; -; Genomic_DNA.
DR PIR; I48717; I48717.
DR HGSP; P05121; IDB2.
DR Ensembl; ENSMUSG0000026249; Mus musculus.
DR MGI; MGI:101780; Serpine2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000215; Prot_inh_serpin.
DR PANTHER; PTHR11461; Prot_inh_serpin; 1.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Developmental protein; Differentiation; Glycoprotein; Heparin-binding;
KW Neurogenesis; Protease inhibitor; Serine protease inhibitor; Serpin;
KW Signal.
FT CHAIN 1 19 By similarity.
FT SITE 20 397 Glia derived nexin.
FT SITE 364 365 Reactive bond (By similarity).
FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
FT CONFLICT 313 313 I -> V (in Ref. 2).
SQ SEQUENCE 397 AA; 44207 MW; B8EBAE3CA899D4A5 CRC64;
Query Match 38.5%; Score 796.5; DB 1; Length 397;
Best Local Similarity 43.0%; Pred. No. 1.9e-55;
Matches 159; Conservative 74; Mismatches 134; Indels 3; Gaps 2;
Qy 34 LASDFGVRVFOQVAQASKDRNVVSPYGVASVLAMLOLTGTGETOQQIQAAAGFKIDDKG 93
Db 30 LGSNTGIQVFNQIIRKPHENVVSPHGIASILGLMLQGLGADGKTKQLSTVMRYNVN--G 87
Qy 94 MAPALRHLYKELMGPKWKNKDEISTTDAIFQVORDKLKVGFMFHFPLRSTVKQVDFSEVE 153
Db 88 VGKVLKKINKAIVSKKNDIVTVANAVFLRNGFKHVEFVAVRNKDVPOCEVQNVNFQDPA 147
Qy 154 RARFIINDWVTKHTKGMISNLGKAVD-QLTRVLVNLALYFNGOWKTPFPDSSTHRLFL 212
Db 148 SASSEINFWKTRGMDINLNLSDIGALTRLVNLVAVFKGLMKSRFPQESTKRTF 207
Qy 213 HKSDGSTSVSPVMAQTNKFNYTEFTPDGHYVDILELPHYGDITLSMFTAAPYKEVPLSA 272
Db 208 VAGDGKSQVPMALQSLVSFRSGSTRTPNGLWYNFELPHYGESISMLIALPTESSTPLSA 267
Qy 273 LTNLSAQLISHWKNMTRLPRLVLPKFSLETEVDLKRPLENLGMDTMRQFQADFTSL 332
Db 268 IIPHTTKTIDSMWNTWPKRMQLVLPKFTAVAOQDLKPLKALGITEMFEPSEKAFNFKI 327
Qy 333 SDQELHVAQAQKQKIVNESCTVASSSTAVIVSARMAPESIIIMDRPFLFVVRHNPTQT 392
Db 328 TRSESLHVSHLQAKIEVSESDGTAKASAAATTAIIARSSPPWFIIVDRPFLFSIRINPTGA 387
Qy 393 VLFMGQVMPEP 402
Db 388 ILFLGQVKNP 397
RESULT 13
Q543R5_MOUSE PRELIMINARY; PRT; 397 AA.
AC Q543R5_MOUSE PRELIMINARY; PRT; 397 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 16-days embryo head cDNA, RIKEN full-length enriched library,
clone: C130010H12 product: serine (or cysteine) proteinase inhibitor,
clade E (nexin, plasminogen activator inhibitor type 1), member 2,
full insert sequence (12 days embryo spinal ganglion cDNA, RIKEN full-
length enriched library, clone: D130035K01 product: serine (or cysteine)
proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor
type 1), member 2, full insert sequence) (Adult male corpora
quadrigena cDNA, RIKEN full-length enriched library,


```
QY 273 LTNILSAQLISHWKNMTRPRLVLPKFSLETEVDLRKPLENLGMDMPROFQADFTSL 332
Db 268 IIPHTTKTIDSMWNTWPKMQLVLPKFTAVAQTDLKEPLKALGITEMFEPSKANTKI 327
QY 333 SDQEPHVAQALQKQKIEVNESGTVASSTAVIVSARMAPEEIIIMDRPFLFVVRNPTGT 392
Db 328 TRSESLVSHILOKAKIEVSESDGTKASAAATAILIARSSPPWFIVDRPFLFSIRHNPTGA 387
QY 393 VLFMGQVMEP 402
Db 388 ILFLGQVKNP 397

RESULT 14
Q4FJUL_MOUSE PRELIMINARY; PRT; 397 AA.
AC Q4FJUL_MOUSE
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE Serpine2 protein.
GN Name=Serpine2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA Mollenhauer J., Wiemann S., Schick M., Korn B.
RT "Cloning of mouse full open reading frames in Gateway (R) system entry
RL vector (pDONR201).";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT010311; CAJ18519.1; -; mRNA.
SQ SEQUENCE 397 AA; 44193 MW; F7F5413CBEE36863 CRC64;

Query Match 38.5%; Score 796.5; DB 2; Length 397;
Best Local Similarity 43.0%; Pred. No. 1.9e-55;
Matches 159; Conservative 74; Mismatches 134; Indels 3; Gaps 2;

QY 34 LASDFGVRFQVQAQSKDRNVVFPYGVASVLAQLTTGCTGCTQQQIQAAAGFKIDDKG 93
Db 30 LGSNTGIVFNQIIKSRPHENVVSPHGIASILGLMLQLGADGRTKKQLSTVNRVNV--G 87

QY 94 MAPALRLHYKELMGPNKDEISTTDAIFVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVE 153
Db 88 VGVKLVKINKAIVSKKNDIVTVANAVFLRNGFKMEVPAVRNKDVFCQEVQNVNFQDPA 147

QY 154 RARFINDVWVTKTGKIMISNLGKGAVD-QLTRVLVNLALYNGQWKTFPPDSSTHRLFL 212
Db 148 SASSEINFVWVKNETRGMDINLSPNLDIGALTRVLVNAVYPKGLWKSFRQPESTKKRTF 207

QY 213 HKSDGTSVSPVMAQTNKENTYFTPDGHYDILELPVHGDTLSMFLAAPYKEKVPLSA 272
Db 208 VAGDGKSYQVPMQLAUSVRSSTRTPNGLWTFNFPYHGESIMLIALPTESSTPLSA 267

QY 273 LTNILSAQLISHWKNMTRPRLVLPKFSLETEVDLRKPLENLGMDMPROFQADFTSL 332
Db 268 IIPHTTKTIDSMWNTWPKMQLVLPKFTAVAQTDLKEPLKALGVTEMFEPSKANFTKI 327

QY 333 SDQEPHVAQALQKQKIEVNESGTVASSTAVIVSARMAPEEIIIMDRPFLFVVRNPTGT 392
Db 328 TRSESLVSHILOKAKIEVSESDGTKASAAATAILIARSSPPWFIVDRPFLFSIRHNPTGA 387

QY 393 VLFMGQVMEP 402
Db 388 ILFLGQVKNP 397

STANDARD; PRT; 397 AA.
```

RESULT 15

GDN_RAT

ID_GDN_RAT

```
AC P07092;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glia derived nexin precursor (GDN) (Protease nexin 1) (PN-1).
GN Name=Serpine2; Synonyms=Pl7, Pn1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sommer J., Gloor S.M., Rovelli G.F., Hofsteenge J., Nick H., Meier R.,
RA Monard D.;
RT "CDNA sequence coding for a rat glia-derived nexin and its homology to
RL members of the serpin superfamily.";
RL Biochemistry 26:6407-6410(1987).
[2]
RP PROTEIN SEQUENCE OF 82-96; 165-178 AND 317-333, AND HEPARIN BINDING.
RX PubMed=1554734;
RA Rovelli G., Stone S.R., Guidolin A., Sommer J., Monard D.;
RT "Characterization of the heparin-binding site of glia-derived
RL nexin/protease nexin-1.";
RL Biochemistry 31:3542-3549(1992).
[3]
RP PROTEIN SEQUENCE OF 133-153 AND 347-397, AND FUNCTION.
RX MEDLINE=90248459; PubMed=2337608;
RA Nick H., Hofsteenge J., Shaw E., Rovelli G., Monard D.;
RT "Functional sites of glia-derived nexin (GDN): importance of the site
RL reacting with the protease.";
RL Biochemistry 29:2417-2421(1990).
CC -!- FUNCTION: Serine protease inhibitor with activity toward thrombin,
CC trypsin, and urokinase. Promotes neurite extension by inhibiting
CC thrombin. Binds heparin.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to the serpin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR EMBL; M17784; AAA41209.1; -; mRNA.
DR PIR; B27496; B27496.
DR HSSP; P05121; 1DB2.
DR RGD; 3748; Serpine2.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; TAS.
DR InterPro; IPR000215; Prot_inh_serpin.
DR PANTHER; PTHR11461; Prot_inh_serpin; 1.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SRPIN; 1.
KW Developmental protein; Differentiation; Direct protein sequencing;
KW Glycoprotein; Heparin-binding; Neurogenesis; Protease inhibitor;
KW Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 397 Glia derived nexin.
FT SITE 364 365 Reactive bond (Potential).
FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 397 AA; 44063 MW; 11EF0790C7297646 CRC64;

Query Match 38.2%; Score 791.5; DB 1; Length 397;
Best Local Similarity 42.7%; Pred. No. 4.8e-55;
Matches 158; Conservative 72; Mismatches 137; Indels 3; Gaps 2;

QY 34 LASDFGVRFQVQAQSKDRNVVFPYGVASVLAQLTTGCTGCTQQQIQAAAGFKIDDKG 93
Db 30 LGSNTGIVFNQIIKSRPHENVVSPHGIASILGLMLQLGADGRTKKQLSTVNRVNV--G 87

QY 94 MAPALRLHYKELMGPNKDEISTTDAIFVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVE 153
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Db	88	VGKVLKKINKAIVSKKNKDI	VIVANAVFVRNGFKVEVPFAARNKEVFQCEVQSVNFQDDPA	147
Qy	154	RAREFIINDWVKTHTKGMI	SNLLGKGAVDQ-LTRLVLVNALYFNGQWKTPFPDSSSTRRLF	212
Db	148	SACDAINFVVKNETRGMI	DNLNLLSPNLIDSLTKLVLVNAVYFKGLWKSRRQOPENTKKRTF	207
Qy	213	HKSDGSTVSVPMMAQT	NKFNTEFTPDGHHYDILELPYHGDTLSMFIAAPYEKEVEPLSA	272
Db	208	VAGDGKSYQVPM	LAQLSVFRSGSTKTPNGLWYNFIELPYHGESISMLIALFTESSTPLSA	267
Qy	273	LTNILSAQLISHWKGN	TRLPRLLVLPKFSLETEVDLRKPLENLGWTDMRQFOADFTSL	332
Db	268	IIPHISTKIINSWMNT	WPKRMQLVLPKFTALAQTDLKEPLKALGITEMFEPSKANFAKI	327
Qy	333	SDQBPLHVAQALQVK	IEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLFVVRHNPTGT	392
Db	328	TRSESLHVSHILQAK	IEVSEDTKAAVVTTAILIARSSPPWFIVDRPFLFCIRHNPTGA	387
Qy	393	VLFMGQVMEP	402	
Db	388	ILFLGQVKNP	397	

Search completed: December 13, 2005, 09:08:39
Job time : 235 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2005, 15:46:54 ; Search time 189 Seconds
(without alignments)
934.552 Million cell updates/sec

Title: US-10-506-406-2
Perfect score: 2071
Sequence: 1 MQMSPALTLVLGLALVGE.....FVVRHPTGTVLFGQWMEP 402

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2071	100.0	402	AAW31587	Aaw31587 Human pla
2	2071	100.0	402	AAU04913	Aau04913 Human pla
3	2071	100.0	402	AAB90794	Aab90794 Human she
4	2071	100.0	402	ABP65137	Abp65137 Hypoxia-r
5	2071	100.0	402	AAE14271	Aae14271 Plasminog
6	2071	100.0	402	ABP68605	Abp68605 Human pan
7	2071	100.0	402	AAE37131	Aae37131 Human pla
8	2071	100.0	402	ABR82199	AbR82199 Human pla
9	2071	100.0	402	ABR63123	AbR63123 Human pla
10	2071	100.0	402	ADF28929	Adf28929 Human pla
11	2071	100.0	402	ADF28771	Adf28771 Human pla
12	2071	100.0	402	ABW02690	Abw02690 Human pla
13	2071	100.0	402	ADN95544	Adn95544 Human BRC
14	2071	100.0	402	ADJ75605	Adj75605 Marker ge
15	2071	100.0	402	ADL35812	Adl35812 Human pla
16	2071	100.0	402	ADO05046	Ado05046 Human pla
17	2071	100.0	402	ABW80915	Abw80915 Tumour-as
18	2071	100.0	402	ADP23374	Adp23374 PRO polyP
19	2071	100.0	402	ADQ39257	Adq39257 Human myo
20	2071	100.0	402	ADQ39256	Adq39256 Human myo
21	2071	100.0	402	ADV70216	Adv70216 Tumour-as
22	2071	100.0	402	AEA81039	Aea81039 Human pla
23	2071	100.0	402	AEB29725	Aeb29725 Human Ser
24	2067	99.8	402	AAR07986	Aar07986 Plasminog

Aar23812 PAI-1 (Ar
Aar23813 PAI-1 (Ar
Ade48115 Human PAI
Aap81179 Sequence
Abm83091 Human dia
Abm83092 Human dia
Abr63124 Human pla
Aap82007 Beta plas
Aau97221 Wild-type
Aaw26718 Plasminog
Aau04926 Human pla
Aar08411 Modified
Aaw26717 Plasminog
Aau04925 Human pla
Aaw26714 Plasminog
Aau04922 Human pla
Aaw26710 Plasminog
Aau04918 Human pla
Aau97224 Human PAI
Aau97230 Human PAI
Aau97229 Human PAI

ALIGNMENTS

RESULT 1
AAW31587
ID AAW31587 standard; protein; 402 AA.
XX AC AAW31587;
XX AC
XX DT 14-APR-1998 (first entry)
XX DE Human plasminogen activator inhibitor type 1.

XX KW Plasminogen activator inhibitor type 1; PAI-1; human; elastase inhibitor;
XX KW vitronectin; cell attachment; cell migration; cell proliferation;
XX KW emphysema; adult respiratory distress syndrome; acute lung inflammation;
XX KW alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis;
XX KW pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis;
XX KW restenosis; neointima; fibrosis; wound healing; tumour; metastasis;
XX KW psoriasis; thrombosis; angiogenesis; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT Protein /label= Sig_peptide
XX FT Protein /label= Mat protein
XX FT Misc-difference 173 /note= "preferred substitution site for protein stabilisation"
XX FT Misc-difference 177 /note= "preferred substitution site for protein stabilisation"
XX FT Misc-difference 342 /note= "preferred substitution site for protein stabilisation"
XX FT Region 354..375 /note= "reactive centre loop region"
XX FT Misc-difference 366 /label= P4
XX FT /note= "preferred substitution site to provide elastase inhibitor mutant"
XX FT Misc-difference 369 /label= P1
XX FT /note= "preferred substitution site to provide elastase inhibitor mutant"
XX FT Misc-difference 377 /note= "preferred substitution site for protein

```
FT XX substitution"
PN XX
XX MO9739028-A1.
XX
XX 23-OCT-1997.
XX
XX 11-APR-1997; 97WO-US006071.
XX
XX 12-APR-1996; 96US-0015299P.
XX
XX (AMNA-) AMERICAN NAT RED CROSS.
XX
XX Lawrence DA, Stefansson SP;
XX
XX WPI; 1997-526399/48.
XX N-PSDB; AAT97303.
XX
XX Plasminogen activator-inhibitor type I mutant inhibits elastase - or has
XX high affinity for vitronectin, for therapeutic inhibition of elastase or
XX vitronectin-mediated cell attachment, migration etc.
XX
XX Claim 3; Fig 4A; 144pp; English.
XX
XX This polypeptide sequence comprises wild-type human plasminogen activator
XX inhibitor type (PAI-1). Novel mutants (see AAM26710-25) of the PAI-1
XX mature protein are claimed that inhibit elastase or other elastase-like
XX proteases, or are inhibitors of vitronectin-dependent cell migration. The
XX mutants are obtained by site-directed mutagenesis of the PAI-1 DNA
XX sequence (see AAT97303) and expression in host cells, and have a range of
XX therapeutic uses. Preferred mutants have amino acid substitutions in the
XX reactive centre loop region (especially at position 343 and/or 346 of the
XX mature protein), and may have additional stabilising amino acid
XX substitutions at 1-4 of residues 150, 154, 319 and 354, and 1-5 of
XX residues 333, 335, 371, 372 and 91
XX
XX Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQMSPALTCLVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQAKDRNVFSPY 60
DB 1 MQMSPALTCLVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQAKDRNVFSPY 60
QY 61 GVASVLAMQLTTGGETQQQIQAAAGFKIDDKGMAPALRHLKELMGFPWKNDEISTTDAI 120
DB 61 GVASVLAMQLTTGGETQQQIQAAAGFKIDDKGMAPALRHLKELMGFPWKNDEISTTDAI 120
QY 121 FVQRDLKLVQGFMPHPRFRSTYKQVDFSEVERPFIINDWVTKTKGMISNLLKGAV 180
DB 121 FVQRDLKLVQGFMPHPRFRSTYKQVDFSEVERPFIINDWVTKTKGMISNLLKGAV 180
QY 181 DQLTRLVLVNALYNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAOTNKFNYTEFTTPD 240
DB 181 DQLTRLVLVNALYNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAOTNKFNYTEFTTPD 240
QY 241 GHYYDILELPHVGTLSMFTAAPEYKEVPLSALTNILSAQLISHKWNMTLRPLLLVLPK 300
DB 241 GHYYDILELPHVGTLSMFTAAPEYKEVPLSALTNILSAQLISHKWNMTLRPLLLVLPK 300
QY 301 FSLETEVDLRKPLENLTDMFROFQADFTSLSDQEPHLHVAQALOKYKIEVNESGTVA 360
DB 301 FSLETEVDLRKPLENLTDMFROFQADFTSLSDQEPHLHVAQALOKYKIEVNESGTVA 360
QY 361 STAVIVSARMAPEIIMDRPFLFVRNPTGTVLFMGQVMEP 402
DB 361 STAVIVSARMAPEIIMDRPFLFVRNPTGTVLFMGQVMEP 402

RESULT 2
AAU04913
ID AAU04913 standard; protein; 402 AA.

AAU04913;
26-SEP-2001 (first entry)
Human Plasminogen activator inhibitor-1, PAI-1.
Human; Plasminogen activator inhibitor-1; PAI-1; serpin;
immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome;
ARDS; HIV infection; Human immunodeficiency virus; prostate cancer;
TNF-mediated inflammation; benign prostatic hypertrophy.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..23
/label= Signal_peptide
/Note= "Alternative signal peptide"
Peptide 1..21
/label= Signal_peptide
/Note= "Alternative signal peptide"
Protein 22..402
/label= Mature_PAI-1 #1
Protein 24..402
/label= Mature_PAI_1 #2
Region 357..374
/label= Reactive_centre_loop
WO200138560-A2.
31-MAY-2001.
22-NOV-2000; 2000MO-US032315.
22-NOV-1999; 99US-0167553P.
(AMNA-) AMERICAN NAT RED CROSS.
Lawrence DA, Day D;
WPI; 2001-441438/47.
N-PSDB; AAS09460.
Detecting a functionally active form of an enzyme in a biological sample
comprises contacting an enzyme inhibitor immobilized on a solid
substrate.
Disclosure; Fig 5; 69pp; English.
The sequence represents human plasminogen activator inhibitor-1, PAI-1, a
serine proteinase inhibitor or serpin. The protein is used to demonstrate
the method of the invention which comprises detecting a functionally
active form of an enzyme in a biological sample by contacting an enzyme
inhibitor immobilised on a solid substrate with the biological sample and
measuring the binding of the enzyme inhibitor to the active form of the
enzyme by a detectable label, where the enzyme inhibitor specifically
forms a covalent bond or binds with a dissociation constant of 1 x 10-9M
or less with the active form of the enzyme. The present invention
provides a sensitive method for the detection of a functionally active
form of an enzyme in a biological sample. Human PAI-1 can be used to
detect a number of enzymes including tissue plasminogen activator,
urokinase, thrombin, plasmin, neutrophil elastase, pancreatic elastase,
trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as
such can be used in methods to diagnose diseases such as cystic fibrosis,
acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated
inflammation, prostate cancer and benign prostatic hypertrophy
XX
XX Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHILASDFGVRVFOOVAQAKDRNVVFSY 60
DB 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHILASDFGVRVFOOVAQAKDRNVVFSY 60
QY 61 GVASVLAMQLTTCGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120
DB 61 GVASVLAMQLTTCGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120
QY 121 FVQDRLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
DB 121 FVQDRLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
QY 181 DQTRRLVLNLYFNGQWKTFFPDSSTHRLFHKSDDGSTVSPVMAQTNKFNTEFTTPD 240
DB 181 DQTRRLVLNLYFNGQWKTFFPDSSTHRLFHKSDDGSTVSPVMAQTNKFNTEFTTPD 240
QY 241 GHYDILLELPYHGDTLNFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
DB 241 GHYDILLELPYHGDTLNFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
QY 301 FSLETEVDLRKPLENLGMDTFROFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
DB 301 FSLETEVDLRKPLENLGMDTFROFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
QY 361 STAVIVSARMAPEEIIIMDRPELFVVRHNPTGTVLFMGQVMEP 402
DB 361 STAVIVSARMAPEEIIIMDRPELFVVRHNPTGTVLFMGQVMEP 402

RESULT 3
AAB90794
ID AAB90794 standard; protein; 402 AA.

AC AAB90794;
XX
XX
DT 15-JUN-2001 (first entry)
DE Human shear stress-response protein; protein; 402 AA.
DE Human shear stress-response protein; protein; 402 AA.
KW Human; shear stress-response protein; protein; 402 AA.
OS Homo sapiens.
XX
XX WO200125427-A1.
XX 12-APR-2001.
XX 02-OCT-2000; 2000WO-JP006840.
XX 01-OCT-1999; 99JP-00280976.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX (NOJII) NOJIMA H.
XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX WPI; 2001-266308/27.
XX N-PSDB; AA02917.
XX
XX DNA sequences, proteins encoded by them and antibodies against them
XX useful in diagnosis and treatment of vascular disease caused by
XX arteriosclerosis.
XX
XX Claim 60; Page 476-478; 678pp; Japanese.

XX The present invention provides the protein and coding sequences of a
XX number of human shear stress response proteins. These are useful in the
XX diagnosis, treatment and screening of vascular diseases caused by
XX arteriosclerosis, including heart failure, post-PTCA restenosis and
XX hypertension

SQ Sequence 402 AA;
Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHILASDFGVRVFOOVAQAKDRNVVFSY 60
DB 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHILASDFGVRVFOOVAQAKDRNVVFSY 60
QY 61 GVASVLAMQLTTCGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120
DB 61 GVASVLAMQLTTCGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120
QY 121 FVQDRLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
DB 121 FVQDRLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
QY 181 DQTRRLVLNLYFNGQWKTFFPDSSTHRLFHKSDDGSTVSPVMAQTNKFNTEFTTPD 240
DB 181 DQTRRLVLNLYFNGQWKTFFPDSSTHRLFHKSDDGSTVSPVMAQTNKFNTEFTTPD 240
QY 241 GHYDILLELPYHGDTLNFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
DB 241 GHYDILLELPYHGDTLNFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
QY 301 FSLETEVDLRKPLENLGMDTFROFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
DB 301 FSLETEVDLRKPLENLGMDTFROFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
QY 361 STAVIVSARMAPEEIIIMDRPELFVVRHNPTGTVLFMGQVMEP 402
DB 361 STAVIVSARMAPEEIIIMDRPELFVVRHNPTGTVLFMGQVMEP 402

RESULT 4
ABP65137
ID ABP65137 standard; protein; 402 AA.
XX
XX AC ABP65137;
XX
XX DT 12-NOV-2002 (first entry)
XX Hypoxia-regulated protein #11.
XX
XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW preclampsia; atherosclerosis; inflammatory condition; wound healing;
KW inflammation; erythropoiesis; hair loss; human.
XX
XX Homo sapiens.
XX
XX WO200246465-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 10-DEC-2001; 2001WO-GB005458.
XX
XX PR 08-DEC-2000; 2000GB-00030076.
XX PR 08-FEB-2001; 2001GB-00003156.
XX PR 25-OCT-2001; 2001GB-00025666.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX PI White J, Mundy CR, ward NR, Krige D, Kingsman SM, Harris RA;
XX Rayner WN;
XX
XX WPI; 2002-627238/67.
XX
XX Identifying a gene involved in disease for treating hypoxia-regulated
XX conditions, comprises comparing the transcriptome/proteome of two cell
XX

PT types under different conditions and identifying a differentially
 PT regulated gene.
 XX
 PS Claim 35; Page 338; 538pp; English.
 XX
 CC The present invention relates to methods for identifying genes and
 CC proteins that are implicated in a specific disease or physiological
 CC condition. The method comprises comparing the transcriptome/proteome of a
 CC specialised cell type implicated in a disease or condition with that of a
 CC second specialised cell type, under two experimental conditions, and
 CC identifying a gene that is differentially regulated in the two
 CC specialised cell types under experimental conditions. ABV77873-ABV78116
 CC and ABP65061-ABP65257 were identified using the methods of the invention.
 CC The coding sequences and proteins are useful for treating a disease in a
 CC patient, for manufacture of a medicament for treating hypoxia-regulated
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
 CC biological response to hypoxia conditions, or hypoxic-associated
 CC pathology in a patient. The coding sequences and proteins are also useful
 CC for monitoring the therapeutic treatment of a disease or physiological
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,
 CC retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss
 XX
 SQ Sequence 402 AA;
 Query Match 100.0%; Score 2071; DB 5; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQSKDRNVFSPY 60
 DB 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQSKDRNVFSPY 60
 QY 61 GVASVLAMQLTGTGGETQQOIQAAAGFKIDDKGMAPALRHLHYKELMGPNKDEISTTDAI 120
 DB 61 GVASVLAMQLTGTGGETQQOIQAAAGFKIDDKGMAPALRHLHYKELMGPNKDEISTTDAI 120
 QY 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHGMISNLLGKAV 180
 DB 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHGMISNLLGKAV 180
 QY 181 DQTRLVLVNALYFNGQWKTPFPDSSTHRLRFLFKSDGSTVSPVMAQTNKFNTEFTTPD 240
 DB 181 DQTRLVLVNALYFNGQWKTPFPDSSTHRLRFLFKSDGSTVSPVMAQTNKFNTEFTTPD 240
 QY 241 GHYVDILELPYHGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRPLLLVLPK 300
 DB 241 GHYVDILELPYHGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRPLLLVLPK 300
 QY 301 FSLSEVDLRKPLENLGMDTDFRQFQADFTSLSDQEPPLHVAQALQKVKIEVNESGTVA 360
 DB 301 FSLSEVDLRKPLENLGMDTDFRQFQADFTSLSDQEPPLHVAQALQKVKIEVNESGTVA 360
 QY 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402
 DB 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402
 RESULT 5
 ID AAE14271
 AC AAE14271
 XX AAE14271;
 AC AAE14271;
 DT 07-AUG-2003 (revised)
 DT 07-MAR-2002 (first entry)
 XX
 XX Plasminogen activator inhibitor (PAI) 1.
 XX
 KW Pancreas-derived plasminogen activator inhibitor; PAI;
 KW plasminogen activator inhibitor; PAI; preeclampsia; wound healing;
 KW intrauterine growth retardation; tumour cell invasion; arthritis;
 KW metastasis; inflammation; inflammatory bowel disease; appendicitis;

KW systemic lupus erythematosus; ovulation; cytostatic; gene therapy;
 KW prostatic involution; osteonecrosis; breast cancer; pregnancy.
 XX Unidentified.
 OS US6303338-B1.
 PN 16-OCT-2001.
 XX 19-FEB-1998; 98US-00026408.
 XX 16-AUG-1996; 96US-0024056P.
 PR 15-AUG-1997; 97US-00934011.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ni J, Gentz RL, Ruben SM, Shi YE;
 XX WPI; 2002-033216/04.
 XX Isolated polynucleotides encoding the pancreas-derived plasminogen
 PT activator inhibitor protein are useful to treat physiological and
 PT pathological conditions including breast cancer, and to detect
 PT pathological disorders.
 XX
 PS Disclosure; Fig 2; 50pp; English.
 XX The invention relates to nucleic acids encoding pancreas-derived
 CC plasminogen activator inhibitor (PAI) protein. Plasminogen activator
 CC inhibitor (PAI) 1 and 2 are involved in many physiological and
 CC pathological processes, including normal pregnancy, preeclampsia,
 CC intrauterine growth retardation, wound healing, tumour cell invasion and
 CC metastasis, inflammation and arthritis, inflammatory bowel disease,
 CC and prostatic involution and osteonecrosis. PAI1 DNA is used to treat
 CC physiological and pathological conditions including breast cancer and to
 CC detect pathological disorders. PAI1 DNA is used in gene therapy. The
 CC present amino acid sequence is a PAI protein. (Updated on 07-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 402 AA;
 Query Match 100.0%; Score 2071; DB 5; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQSKDRNVFSPY 60
 DB 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQSKDRNVFSPY 60
 QY 61 GVASVLAMQLTGTGGETQQOIQAAAGFKIDDKGMAPALRHLHYKELMGPNKDEISTTDAI 120
 DB 61 GVASVLAMQLTGTGGETQQOIQAAAGFKIDDKGMAPALRHLHYKELMGPNKDEISTTDAI 120
 QY 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHGMISNLLGKAV 180
 DB 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHGMISNLLGKAV 180
 QY 181 DQTRLVLVNALYFNGQWKTPFPDSSTHRLRFLFKSDGSTVSPVMAQTNKFNTEFTTPD 240
 DB 181 DQTRLVLVNALYFNGQWKTPFPDSSTHRLRFLFKSDGSTVSPVMAQTNKFNTEFTTPD 240
 QY 241 GHYVDILELPYHGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRPLLLVLPK 300
 DB 241 GHYVDILELPYHGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTLRPLLLVLPK 300
 QY 301 FSLSEVDLRKPLENLGMDTDFRQFQADFTSLSDQEPPLHVAQALQKVKIEVNESGTVA 360
 DB 301 FSLSEVDLRKPLENLGMDTDFRQFQADFTSLSDQEPPLHVAQALQKVKIEVNESGTVA 360
 QY 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402
 DB 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402

RESULT 6
 ABP68605
 ID ABP68605 standard; protein; 402 AA.
 AC ABP68605;
 XX
 DT 14-JAN-2003 (first entry)
 DE Human pancreatic cancer expressed protein SEQ ID NO 154.
 KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytostatic; tumour.
 OS Homo sapiens.
 XX
 PN WO200260317-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-US002781.
 XX
 PR 30-JAN-2001; 2001US-0265305P.
 PR 31-JAN-2001; 2001US-0265682P.
 PR 09-FEB-2001; 2001US-0267568P.
 PR 21-MAR-2001; 2001US-0278651P.
 PR 28-APR-2001; 2001US-0287112P.
 PR 16-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 DR WPI; 2002-627435/67.
 DR N-PSDB; ABV94750.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 154; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 402 AA;
 Query Match 100.0%; Score 2071; DB 5; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQMSPALTCLVLGLALVFGSGSAVHPSPSVVAHLASDFGVRVFPQQAQSKORNVVFSY 60
 DB 1 MQMSPALTCLVLGLALVFGSGSAVHPSPSVVAHLASDFGVRVFPQQAQSKORNVVFSY 60

61 GVASVLAMQLTTGGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
 DB 61 GVASVLAMQLTTGGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
 QY 121 FVQRDLKLVOGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
 DB 121 FVQRDLKLVOGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
 QY 181 DQTLRLVLVNALYFNGQKTFPPDSSTHRRLFHKS DGSSTVSPMMAQTNKENYTFETTPD 240
 DB 181 DQTLRLVLVNALYFNGQKTFPPDSSTHRRLFHKS DGSSTVSPMMAQTNKENYTFETTPD 240
 QY 241 GHYDILLELPYHGDTLNLSAQLISHWKGNMTRPRLLLVLPK 300
 DB 241 GHYDILLELPYHGDTLNLSAQLISHWKGNMTRPRLLLVLPK 300
 QY 301 FSLETEVDLRKPLENLGMDTFROFQADFTSLSDQEPHLHVAQLOKVKIEVNESGTVA 360
 DB 301 FSLETEVDLRKPLENLGMDTFROFQADFTSLSDQEPHLHVAQLOKVKIEVNESGTVA 360
 QY 361 STAVIVSARMAPESIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 DB 361 STAVIVSARMAPESIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 7
 AAE37131
 ID AAE37131 standard; protein; 402 AA.
 AC AAE37131;
 XX
 DT 07-AUG-2003 (first entry)
 DE Human plasminogen-activator inhibitor type 1 (PAI-1) protein.
 KW Osteoarthritis; rheumatoid arthritis; plasmin; plasminogen; human;
 KW urokinase-type plasminogen activator; uPA; degenerative joint disease;
 KW spondyloarthropathy; antisense-therapy; antibody therapy; osteopathic;
 KW urokinase-type plasminogen activator receptor; psoriatic arthritis;
 KW plasminogen-activator inhibitor type 1; PAI-1; uPAR.
 OS Homo sapiens.
 XX
 PN WO2003033009-A2.
 XX
 PD 24-APR-2003.
 PF 10-JUL-2002; 2002WO-IB005797.
 PR 10-JUL-2001; 2001US-0304461P.
 PR 10-JUL-2001; 2001US-0304490P.
 PR 13-JUL-2001; 2001US-0305182P.
 XX (OMNI-) OMNIO AB.
 XX
 PI Ny T, Holmdahl R, Li J;
 XX WPI; 2003-393477/37.
 DR N-PSDB; AAD56136.
 XX
 PT Treating or preventing arthritis e.g. osteoarthritis, rheumatoid
 PT arthritis in mammals, by administering inhibitors of plasmin,
 PT plasminogen, urokinase-type plasminogen activator or plasminogen-
 PT activator inhibitor type 1.
 XX
 PS Disclosure; Page 82-83; 85pp; English.
 XX
 CC The invention relates to a method for treating or preventing arthritis
 CC e.g. osteoarthritis, rheumatoid arthritis in mammals, by administering
 CC inhibitors of plasmin, plasminogen, urokinase-type plasminogen activator
 CC (uPA), plasminogen-activator inhibitor type 1 (PAI-1) and urokinase-type
 CC plasminogen activator receptor (uPAR). The method is useful for treating

CC or preventing arthritis caused by degenerative joint disease, preferably
 CC rheumatoid arthritis, psoriatic arthritis, infectious arthritis, juvenile
 CC rheumatoid arthritis, osteoarthritis and spondyloarthropathies in a
 CC mammal, especially a human. It is also useful for identifying agents for
 CC treating or preventing arthritis in a mammal and it is also useful in
 CC antisense-therapy and antibody therapy. The present sequence is human PAI
 CC -1 protein
 XX
 SQ Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 6; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGGSAVHPPSYVAHLASDFGVRVFOQAQASKDRNVVFSFY 60
 Db 1 MQMSPALTCVLGLALVFGGSAVHPPSYVAHLASDFGVRVFOQAQASKDRNVVFSFY 60
 Qy 61 GVASVLAMQLTTGGTQQQIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
 Db 61 GVASVLAMQLTTGGTQQQIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
 Qy 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVKTHKGMISNLLGKAV 180
 Db 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVKTHKGMISNLLGKAV 180
 Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSSTRRLFHKS DGSSTVSPVMAQTNKNYTEFTTPD 240
 Db 181 DQTRLVLVNALYFNGQWKTFFPDSSSTRRLFHKS DGSSTVSPVMAQTNKNYTEFTTPD 240
 Qy 241 GHYVDILELPYHGDITLSMFIAPYEKVPPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
 Db 241 GHYVDILELPYHGDITLSMFIAPYEKVPPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
 Qy 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLHVAQALQKVKIEVNESGTVA 360
 Db 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLHVAQALQKVKIEVNESGTVA 360
 Qy 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Db 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 8

ABR82199
 ID ABR82199 standard; protein; 402 AA.

XX
 AC ABR82199;

DT 30-SEP-2003 (first entry)

XX Human plasminogen activator inhibitor 1 (PAI-1).

XX Human; plasminogen activator inhibitor; PAI-1; PAI; proteinase inhibitor;
 XX mutant proteinase inhibitor.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= signal
 FT Protein 24..402
 FT /label= PAI-1
 FT /note= "plasminogen activator inhibitor 1"

XX WO2003053921-A2.

XX 03-JUL-2003.

XX 18-JUL-2002; 2002WO-US022822.

XX 18-JUL-2001; 2001US-0305908P.

XX

PA (AMNA-) AMERICAN NAT RED CROSS.

XX Lawrence DA, Gorlatova N, Crandall DL;

XX WPI; 2003-569214/53.

DR N-PSDB; ACF06144.

XX Novel mutant proteinase inhibitor comprising a mutation in an epitope of
 PT amino acid sequence of wild-type proteinase inhibitor, useful for
 PT screening compounds that affect inhibitory activity of the proteinase
 PT inhibitor.

XX Claim 8; Fig 1; 46pp; English.

XX The present invention describes a mutant proteinase inhibitor (I)
 CC comprising a wild-type proteinase inhibitor amino acid sequence with at
 CC least 1 mutation in at least 1 epitope of the amino acid sequence, where
 CC the mutation alters the binding of the mutant proteinase inhibitor to an
 CC anti-proteinase inhibitor antibody as compared to the binding of the wild
 CC -type proteinase inhibitor to the anti-proteinase inhibitor antibody. (I)
 CC is useful for screening at least one compound that affects the activity
 CC of a proteinase inhibitor. (I) is also useful for screening at least one
 CC compound that affects the inhibitory activity of a proteinase inhibitor.
 CC The present sequence represents human plasminogen activator inhibitor 1
 CC (PAI-1), which is used in an example from the present invention

XX Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 6; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGGSAVHPPSYVAHLASDFGVRVFOQAQASKDRNVVFSFY 60
 Db 1 MQMSPALTCVLGLALVFGGSAVHPPSYVAHLASDFGVRVFOQAQASKDRNVVFSFY 60
 Qy 61 GVASVLAMQLTTGGTQQQIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
 Db 61 GVASVLAMQLTTGGTQQQIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
 Qy 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVKTHKGMISNLLGKAV 180
 Db 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVKTHKGMISNLLGKAV 180
 Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSSTRRLFHKS DGSSTVSPVMAQTNKNYTEFTTPD 240
 Db 181 DQTRLVLVNALYFNGQWKTFFPDSSSTRRLFHKS DGSSTVSPVMAQTNKNYTEFTTPD 240
 Qy 241 GHYVDILELPYHGDITLSMFIAPYEKVPPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
 Db 241 GHYVDILELPYHGDITLSMFIAPYEKVPPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
 Qy 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLHVAQALQKVKIEVNESGTVA 360
 Db 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLHVAQALQKVKIEVNESGTVA 360
 Qy 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Db 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 9

ABR63123
 ID ABR63123 standard; protein; 402 AA.

XX
 AC ABR63123;

XX 18-DEC-2003 (first entry)

XX Human plasminogen activator inhibitor-1.

XX plasminogen activator inhibitor-1; PAI-1; human; transgenic;
 KW thrombolytic; antiasthmatic; antiinflammatory; nootropic;

KW	neuroprotective; antidepressant; nephrotropic; vulnery;	
KW	antiseborrheic; dermatological; antiarteriosclerotic; hepatotropic.	
XX		
OS	Homo sapiens.	
PN	WO2003071267-A1.	
XX		
PD	28-AUG-2003.	
XX		
XX	19-FEB-2003; 2003WO-US005008.	
PF	19-FEB-2002; 2002US-0358061P.	
PR		
XX	(UYVA-) UNIV VANDERBILT.	
PA	(DECL/) DECLERCK P J.	
XX		
PI	Declerck PJ, Vaughan DE, Eren M;	
XX		
DR	WPI, 2003-721694/68.	
XX	N-PSDB; ACF79498.	
XX		
PT	Treating a warm-blooded vertebrate animal having a medical condition,	
PT	e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or	
PT	glomerulosclerosis, comprises administering a plasminogen activator	
PT	inhibitor-1 inhibitor.	
XX		
PS	Disclosure; Page 62-64; 91pp; English.	
XX		
CC	The present sequence is the protein sequence of human plasminogen	
CC	activator inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce	
CC	transgenic animals of the invention, useful for screening potential PAI-1	
CC	inhibitors. Such PAI-1 inhibitors can be used to treat a warm-blooded	
CC	vertebrate animal having a medical condition, e.g. alopecia, undesired	
CC	weight loss, Alzheimer's disease, systemic amyloidosis, myelofibrosis,	
CC	glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne,	
CC	atherosclerosis, ageing, or a wound (claimed). A method of testing a	
CC	candidate composition for PAI-1 inhibition activity comprises	
CC	administering the composition to a transgenic animal having a PAI-1 gene	
CC	incorporated into its genome, and observing an ameliorating change in the	
CC	animal indicative of inhibition of PAI-1 activity, the change being an	
CC	improvement of a vascular thrombotic disorder, asthma, chronic	
CC	obstructive pulmonary disease, alopecia, undesired weight loss such as	
CC	anorexia, Alzheimer's disease, systemic amyloid deposition, systemic	
CC	amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness,	
CC	keloids, apocrine cysts, acne, atherosclerosis, ageing,	
CC	hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)	
XX		
SQ	Sequence 402 AA;	
	Query Match 100.0%; Score 2071; DB 7; Length 402;	
	Best Local Similarity 100.0%; Pred. No. 4.4e-190;	
	Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MQMSPALTCVLGLALVFEGSAVHHPPSYVAHLASDFGVRFQVQAQASKDRNVVFSY 60	
DB	1 MQMSPALTCVLGLALVFEGSAVHHPPSYVAHLASDFGVRFQVQAQASKDRNVVFSY 60	
QY	61 GVASVLAMQLTGTGTOQIQAAAGFKIDDKGMAPALRHLYKELGMPWNKDEISTDAI 120	
DB	61 GVASVLAMQLTGTGTOQIQAAAGFKIDDKGMAPALRHLYKELGMPWNKDEISTDAI 120	
QY	121 FVORDLKLVGQMPHFRLFRSTVKQVDFSEVERAFIINDVWTKTKMISNLGKGV 180	
DB	121 FVORDLKLVGQMPHFRLFRSTVKQVDFSEVERAFIINDVWTKTKMISNLGKGV 180	
QY	181 DQTRVLVNALYFNGOWKTPPDSTHRLFHKS DGVTSVPMMAQTKNFYETTPD 240	
DB	181 DQTRVLVNALYFNGOWKTPPDSTHRLFHKS DGVTSVPMMAQTKNFYETTPD 240	
QY	241 GHYYDILELPYHGDTLSMFAIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLVLPK 300	
DB	241 GHYYDILELPYHGDTLSMFAIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLVLPK 300	

QY	301 FSLTEVDLRKPLENLGMDTDMFRQFQADFTSLSDQBPPLHVAQALQKVKIEVNSGTVA 360	
DB	301 FSLTEVDLRKPLENLGMDTDMFRQFQADFTSLSDQBPPLHVAQALQKVKIEVNSGTVA 360	
QY	361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFGQVMEP 402	
DB	361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFGQVMEP 402	
	RESULT 10	
ADF28929		
ID	ADF28929 standard; protein; 402 AA.	
XX		
AC	ADF28929;	
XX		
DT	12-FEB-2004 (first entry)	
XX		
XX	Human plasminogen activator inhibitor 1 precursor.	
XX		
KW	Human; plasminogen activator inhibitor 1; gene therapy; cytostatic;	
KW	antidiabetic; immunosuppressive; hepatotropic; adeno-associated virus.	
XX		
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Peptide	1..23
FT	Protein	/label= Signal_peptide
FT		24..402 Plasminogen activator inhibitor 1
XX		
XX	WO2003089011-A1.	
PN		
XX	30-OCT-2003.	
PD		
XX	21-APR-2003; 2003WO-US012324.	
PF		
XX	19-APR-2002; 2002US-0374083P.	
PR		
XX	(UYFL) UNIV FLORIDA.	
PA	Atkinson MA, Flotte TR, Song S, Loiler SA;	
XX		
PI	WPI, 2003-845502/78.	
XX		
DR	New adeno-associated viral vector, useful in preparing a composition for	
XX	treating or preventing e.g., cancer, diabetes, or autoimmune, pancreatic	
PT	or liver disease.	
PT		
XX	Example 4; SEQ ID NO 28; 183pp; English.	
PS		
XX	The present sequence is that of human plasminogen activator inhibitor 1	
CC	precursor. This is an example of a therapeutic protein that can be	
CC	encoded by an adeno-associated virus (AAV) vector of the invention. Such	
CC	vectors comprise a promoter operably positioned upstream of a nucleic	
CC	acid encoding a biologically-active therapeutic mammalian serpin or	
CC	cytokine polypeptide, and optionally also include an enhancer sequence	
CC	and a post-transcriptional regulatory sequence. A recombinant AAV virion	
CC	comprising the vector, and a mammalian cell (preferably an endothelial,	
CC	islet, hepatocyte, pancreas, kidney, muscle, spleen, liver, heart, lung,	
CC	or brain cell) comprising the vector are claimed. A claimed composition	
CC	comprises the vector, the recombinant AAV virion, AAV viral particles, or	
CC	the mammalian cell, and is used in cancer, diabetes, autoimmune disease,	
CC	pancreatic disease or liver disease therapy. The composition is also used	
CC	in claimed methods for preventing type I diabetes, and for reducing the	
CC	rate of disease progression of type I diabetes, in a human.	
XX		
SQ	Sequence 402 AA;	
	Query Match 100.0%; Score 2071; DB 7; Length 402;	
	Best Local Similarity 100.0%; Pred. No. 4.4e-190;	
	Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MQMSPALTCVLGLALVFEGSAVHHPPSYVAHLASDFGVRFQVQAQASKDRNVVFSY 60	
DB	1 MQMSPALTCVLGLALVFEGSAVHHPPSYVAHLASDFGVRFQVQAQASKDRNVVFSY 60	
QY	61 GVASVLAMQLTGTGTOQIQAAAGFKIDDKGMAPALRHLYKELGMPWNKDEISTDAI 120	
DB	61 GVASVLAMQLTGTGTOQIQAAAGFKIDDKGMAPALRHLYKELGMPWNKDEISTDAI 120	
QY	121 FVORDLKLVGQMPHFRLFRSTVKQVDFSEVERAFIINDVWTKTKMISNLGKGV 180	
DB	121 FVORDLKLVGQMPHFRLFRSTVKQVDFSEVERAFIINDVWTKTKMISNLGKGV 180	
QY	181 DQTRVLVNALYFNGOWKTPPDSTHRLFHKS DGVTSVPMMAQTKNFYETTPD 240	
DB	181 DQTRVLVNALYFNGOWKTPPDSTHRLFHKS DGVTSVPMMAQTKNFYETTPD 240	
QY	241 GHYYDILELPYHGDTLSMFAIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLVLPK 300	
DB	241 GHYYDILELPYHGDTLSMFAIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLVLPK 300	

Db 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRFQQAQSKDRNVFSPY 60
Qy 61 GVASVLAMQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGFMPHFRLPSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKGV 180
Db 121 FVQRDLKLVQGFMPHFRLPSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKGV 180
Qy 181 DQLTRLVLNVALYFNGQWKTFFPDSSTHRLRFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Db 181 DQLTRLVLNVALYFNGQWKTFFPDSSTHRLRFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Qy 241 GHYVDILELPHVGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTPLRLLVLPK 300
Db 241 GHYVDILELPHVGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTPLRLLVLPK 300
Qy 301 FSLETEVDLRKPLENLGMDTFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGMDTFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFGQVMEP 402
Db 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFGQVMEP 402

RESULT 11
ADF28771
ID ADF28771 standard; protein; 402 AA.
XX
AC ADF28771;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human plasminogen-activator inhibitor-1 (PAI-1).
XX
KW Urokinase-type plasminogen activator; uPA;
KW plasminogen-activator inhibitor-1; PAI-1; breast cancer; tumour;
KW cancer therapy; human.
XX
OS Homo sapiens.
XX
PN WO2003082072-A2.
XX
PD 09-OCT-2003.
XX
PF 13-FEB-2003; 2003WO-US004538.
XX
PR 13-FEB-2002; 2002US-0356928P.
PR 09-AUG-2002; 2002US-0402311P.
XX
PA (HARB/) HARBECK N.
PA (KATE/) KATES R E.
PA (SCHM/) SCHMITT M.
PA (FOEK/) FOEKENS J A.
XX
PI Harbeck N, Kates RE, Schmitt M, Foekens JA;
XX
DR WPI; 2003-803930/75.
DR N-PSDB; ADF28770.
XX

FT Selecting treatments for cancer, specifically breast cancer, based on
PT levels of urokinase and plasminogen-activator inhibitor-1 in tissue.
XX
PS Disclosure; SEQ ID NO 4; 133pp; English.
XX
CC The invention relates to selecting a treatment regime with highest
CC expected benefit to a patient with primary breast cancer. The method
CC involves measuring the levels of urokinase-type plasminogen activator
CC (uPA) and plasminogen-activator inhibitor-1 (PAI-1), or corresponding
CC mRNA, in primary tumour tissue (or a sample); and classifying the patient

CC as low risk (LR) if the uPA level is below a cut-off value of between the
CC 55 th. and 75 th percentile of normalized or analogous uPA in a
CC randomized population of breast cancer patients, and if the PAI-1 level
CC is lower than a cut-off value between the 61 st and 81 st percentile in
CC the same population, or as high risk (HR) if the levels of uPA and PAI-1
CC are above these cut-off values. The treatment of LR (or HR) patients is
CC then selected as one that results in the highest expected benefit in a
CC comparable population of LR (or HR) patients. The method is used: for
CC selection of the most effective therapy, including one designed to
CC prevent relapse; and to predict expected benefit, overall or disease-free
CC survival in patients with cancer, particularly of the breast but also
CC leukemia and plasmacytoma. The method can also be used: to predict the
CC benefit of preventative treatment for relapse of cancer, especially where
CC HR patients are treated with bisphosphonate drugs; for deciding whether
CC or not to administer an aggressive or non-aggressive regime; and for
CC deciding whether or not to administer chemotherapy in combination with
CC hormone therapy (i.e. if the patient is LR, chemotherapy is not
CC administered; in this case HR patients are those who are estrogen- and/or
CC progesterone- receptor positive). The present sequence represents a human
CC PAI-1 polypeptide.
XX
SQ Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 7; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRFQQAQSKDRNVFSPY 60
Db 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRFQQAQSKDRNVFSPY 60
Qy 61 GVASVLAMQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGFMPHFRLPSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKGV 180
Db 121 FVQRDLKLVQGFMPHFRLPSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKGV 180
Qy 181 DQLTRLVLNVALYFNGQWKTFFPDSSTHRLRFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Db 181 DQLTRLVLNVALYFNGQWKTFFPDSSTHRLRFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Qy 241 GHYVDILELPHVGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTPLRLLVLPK 300
Db 241 GHYVDILELPHVGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTPLRLLVLPK 300
Qy 301 FSLETEVDLRKPLENLGMDTFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGMDTFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFGQVMEP 402
Db 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFGQVMEP 402

RESULT 12
ABW02690
ID ABW02690 standard; protein; 402 AA.
XX
AC ABW02690;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human plasminogen activator inhibitor-1 (PAI-1) protein.
XX
KW Plasminogen activator inhibitor-1; PAI-1; cardiovascular disease;
KW fibrotic disease; gene therapy; antiinflammatory; human.
XX
OS Homo sapiens.
XX
PN US2003199463-A1.
XX

PD 23-OCT-2003.
XX 23-APR-2002; 2002US-00128706.
XX 23-APR-2002; 2002US-00128706.
XX (ITES/) ITESCU S.
XX Itescu S;
XX WPI; 2003-852809/79.
XX N-PSDB; AAD64644, AAD64654.
XX New catalytic nucleic acid that hybridizes to and specifically cleaves an
PT mRNA encoding a Plasminogen Activator Inhibitor-1, useful in preparing a
PT composition for treating e.g., cardiovascular or fibrotic disease.
XX Disclosure; SEQ ID NO 6; Opp; English.
XX The present invention relates to a new catalytic nucleic acid that
CC hybridizes to and specifically cleaves an mRNA encoding a plasminogen
CC activator inhibitor-1 (PAI-1). The invention is useful in preparing a
CC composition for treating cardiovascular or fibrotic disease. The
CC invention is also used in gene therapy. The present sequence is human
CC plasminogen activator inhibitor-1 (PAI-1) protein
XX
XX Sequence 402 AA;
XX
XX Query Match 100.0%; Score 2071; DB 7; Length 402;
XX Best Local Similarity 100.0%; Pred. No. 4.4e-190;
XX Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRFQVQAQSKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRFQVQAQSKDRNVVFSY 60
Qy 61 GVASVLAMQLTGTGTOQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTGTGTOQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQDRLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLGKGV 180
Db 121 FVQDRLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLGKGV 180
Qy 181 DQTRLVNLVNLVFNQWKTFFPDSSTHRRLFHKS DGTSTVSPVMAQNKNYTEFTTPD 240
Db 181 DQTRLVNLVNLVFNQWKTFFPDSSTHRRLFHKS DGTSTVSPVMAQNKNYTEFTTPD 240
Qy 241 GHYDILELPYHGDITLSMFIAPYEKEVPLSALTNLISQAQLISHWKGNNTRLPRLVLPK 300
Db 241 GHYDILELPYHGDITLSMFIAPYEKEVPLSALTNLISQAQLISHWKGNNTRLPRLVLPK 300
Qy 301 FSLTEVDLRKPLENLGMDTMRPQADFTSLSDOEPLHVAQALQKVIENESGTVA 360
Db 301 FSLTEVDLRKPLENLGMDTMRPQADFTSLSDOEPLHVAQALQKVIENESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLVVRHNPTGTVLFGQVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLVVRHNPTGTVLFGQVMEP 402
RESULT 13
ADN95544
ID ADN95544 standard; protein; 402 AA.
XX
XX AC ADN95544;
XX 01-JUL-2004 (first entry)
XX Human BCC/LEC-related protein sequence SeqID467.
XX growth; differentiation; blood endothelial cell; BCC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
XX inflammatory disease; cancer metastasis; lymphatic system; human.
OS Homo sapiens.
XX WO2003080640-A1.
XX 02-OCT-2003.
XX 07-MAR-2003; 2003WO-US006900.
XX 07-MAR-2002; 2002US-0363019P.
XX (LUDM-) LUDMIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
XX Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX WPI; 2003-876899/81.
XX N-PSDB; ADN95545.
XX Example 1; SEQ ID NO 467; 176pp; English.
XX This invention relates to a method of differentially modulating the
XX growth or differentiation of blood endothelial cells (BEC) or lymphatic
XX endothelial cells (LEC) comprises contacting endothelial cells with a
XX composition comprising an agent that differentially modulates blood or
XX lymphatic endothelial cells. Treating hereditary lymphoedema comprises
XX identifying a human subject with lymphoedema and with a mutation in at
XX least one allele of a gene encoding a LEC protein, where the mutation
XX correlates with lymphoedema in human subjects, and with the proviso that
XX the LEC protein is not VEGFR-3; and administering to the subject a
XX composition comprising a lymphatic growth agent selected from VEGF-C or
XX VEGF-D polypeptides and polynucleotides. The invention may be useful for
XX the development of compounds with an antiangiogenic, cytostatic,
XX vasotropic or antiinflammatory activity or for gene therapy. The method
XX is useful in modulating the growth or differentiation of blood
XX endothelial cells or lymphatic endothelial cells, in treating hereditary
XX lymphoedema, in screening for an endothelial cell disorder or
XX predisposition to the disorder or in monitoring the efficacy or toxicity
XX of a drug on endothelial cells. The agent is useful in manufacturing a
XX medicament for the differential modulation of blood vessel endothelial
XX cell or lymphatic vessel endothelial cell growth or differentiation. The
XX lymphatic growth agent may also be used in manufacturing a medicament for
XX the treatment of hereditary lymphoedema resulting from a mutation in a
XX LEC gene or of other diseases involving the lymphatic vessels, such as
XX various inflammatory diseases and cancer metastasis via the lymphatic
XX system. The present sequence is that of a human LEC/BEC differentially
XX expressed protein which is related to the method of the invention. Note:
XX This sequence does not appear in the specification but was obtained by
XX the indexer using the source data given in table 14 of the specification.
XX
XX Sequence 402 AA;
XX
XX Query Match 100.0%; Score 2071; DB 7; Length 402;
XX Best Local Similarity 100.0%; Pred. No. 4.4e-190;
XX Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRFQVQAQSKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRFQVQAQSKDRNVVFSY 60
Qy 61 GVASVLAMQLTGTGTOQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTGTGTOQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQDRLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLGKGV 180
Db 121 FVQDRLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLGKGV 180
Qy 181 DQTRLVNLVNLVFNQWKTFFPDSSTHRRLFHKS DGTSTVSPVMAQNKNYTEFTTPD 240
Db 181 DQTRLVNLVNLVFNQWKTFFPDSSTHRRLFHKS DGTSTVSPVMAQNKNYTEFTTPD 240
Qy 241 GHYDILELPYHGDITLSMFIAPYEKEVPLSALTNLISQAQLISHWKGNNTRLPRLVLPK 300
Db 241 GHYDILELPYHGDITLSMFIAPYEKEVPLSALTNLISQAQLISHWKGNNTRLPRLVLPK 300
Qy 301 FSLTEVDLRKPLENLGMDTMRPQADFTSLSDOEPLHVAQALQKVIENESGTVA 360
Db 301 FSLTEVDLRKPLENLGMDTMRPQADFTSLSDOEPLHVAQALQKVIENESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLVVRHNPTGTVLFGQVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLVVRHNPTGTVLFGQVMEP 402
RESULT 13
ADN95544
ID ADN95544 standard; protein; 402 AA.
XX
XX AC ADN95544;
XX 01-JUL-2004 (first entry)
XX Human BCC/LEC-related protein sequence SeqID467.
XX growth; differentiation; blood endothelial cell; BCC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW

Db 181 DQTRLVLVNALYPNGQWTPFPDSSTHRRLFHKSDGTSVSPVPMMAQTNKFNFTTEPTPD 240
 Qy 241 GHYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSAQLISHWKGNTLRLPLLLVLPK 300
 Db 241 GHYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSAQLISHWKGNTLRLPLLLVLPK 300
 Qy 301 FSLETEVDLRKPLENLGWTDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
 Db 301 FSLETEVDLRKPLENLGWTDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
 Qy 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Db 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 14

ADJ75605
 ID ADJ75605 standard; protein; 402 AA.

AC ADJ75605;

XX 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:857.

KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.

XX Homo sapiens.

XX EPI394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX Example 11; SEQ ID NO 857; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of

CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognizing
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 8; Length 402;

Best Local Similarity 100.0%; Pred. No. 4.4e-190;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHLASDFGVRVQQVAQASKDRNVFSPY 60

Db 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHLASDFGVRVQQVAQASKDRNVFSPY 60

Qy 61 GVASVLAMQLQTTGGTQQOIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120

Db 61 GVASVLAMQLQTTGGTQQOIQAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120

Qy 121 FVORDLKLVOGPNPFRFLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLKGAV 180

Db 121 FVORDLKLVOGPNPFRFLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLKGAV 180

Qy 181 DQTRLVLVNALYPNGQWTPFPDSSTHRRLFHKSDGTSVSPVPMMAQTNKFNFTTEPTPD 240

Db 181 DQTRLVLVNALYPNGQWTPFPDSSTHRRLFHKSDGTSVSPVPMMAQTNKFNFTTEPTPD 240

Qy 241 GHYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSAQLISHWKGNTLRLPLLLVLPK 300

Db 241 GHYDILELPHYHGTLSMFTAAPEYKEVPLSALTNILSAQLISHWKGNTLRLPLLLVLPK 300

Qy 301 FSLETEVDLRKPLENLGWTDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360

Db 301 FSLETEVDLRKPLENLGWTDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360

Qy 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

Db 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 15

ADL35812

ID ADL35812 standard; protein; 402 AA.

AC ADL35812;

XX 03-JUN-2004 (first entry)

DE Human plasminogen activator inhibitor 1 (SERPIN1, PAI-1) protein.

KW angiogenesis; cytostatic; cancer; gene therapy; human;

KW plasminogen activator inhibitor 1; SERPIN1; PAI-1.

XX Homo sapiens.

XX WO2004019893-A2.

XX 11-MAR-2004.

XX 02-SEP-2003; 2003WO-US027523.

XX 30-AUG-2002; 2002US-00231956.

XX (RIGE-) RIGEL PHARM INC.

XX Lorens JB, Bogenberger J, Holland S, Xu W;

XX WPI; 2004-239116/22.


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DR N-PSDB; ADL35811.
XX Identifying a compound that modulates angiogenesis for treating e.g.,
PT cancer comprises contacting the compound with a nucleic acid or
PT polypeptide and determining the functional effect of the compound upon
PT the nucleic acid or polypeptide.
XX Claim 19; SEQ ID NO 420; 245pp; English.
PS
XX The invention relates to a novel method for identifying a compound that
CC modulates angiogenesis which comprises contacting the compound with a
CC nucleic acid, or a polypeptide encoded by a nucleic acid, that hybridises
CC under stringent conditions to a second nucleic acid and determining the
CC functional effect of the compound upon the nucleic acid or polypeptide.
CC The method of the invention has cytostatic applications and may be useful
CC for identifying a compound that modulates angiogenesis for treating
CC cancer or for use during gene therapy procedures. The current sequence is
CC that of an angiogenesis-related human protein of the invention.
XX
SQ Sequence 402 AA;
Query Match 100.0%; Score 2071; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSFY 60
DB 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSFY 60
QY 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
DB 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
QY 121 FVQDRLKLVQGMFPHFRFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKGV 180
DB 121 FVQDRLKLVQGMFPHFRFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKGV 180
QY 181 DQTLRLVLNLYFNGQWKTTPDSTHRRLFHKSDGSTVSPVMAQTNKKNYTFETTPD 240
DB 181 DQTLRLVLNLYFNGQWKTTPDSTHRRLFHKSDGSTVSPVMAQTNKKNYTFETTPD 240
QY 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLPK 300
DB 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLPK 300
QY 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
DB 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
QY 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
DB 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
RESULT 16
AD005046
ID AD005046 standard; protein; 402 AA.
XX
AC AD005046;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human plasminogen activator inhibitor (PAI)-1 protein.
XX
XX Plasminogen activator inhibitor; PAI; human.
XX
XX Homo sapiens.
XX
XX US2004086978-A1.
XX
XX 06-MAY-2004.
XX
XX 29-JUL-2003; 2003US-00628395.
XX
XX
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XX 16-AUG-1996; 96US-0024056P.
PR 15-AUG-1997; 97US-00934011.
PR 19-FEB-1998; 98US-00026408.
PR 12-JUL-2001; 2001US-00902884.
XX
PA (NIJJ/) NI J.
PA (GENT/) GENTZ R L.
PA (RUBE/) RUBEN S M.
PA (SHIY/) SHI Y E.
XX
XX NI J, Gentz RL, Ruben SM, Shi YE;
XX WPI; 2004-356204/33.
XX Producing an antibody that specifically binds to pancreas-derived
PT plasminogen activator inhibitor (PAPAI) polypeptide comprises introducing
PT the polypeptide to the animal, and recovering the antibody.
XX
PS Disclosure; SEQ ID NO 3; 51pp; English.
XX
XX The present invention provides pancreas-derived plasminogen activator
CC inhibitor (PAPAI) polypeptides and their encoding polynucleotides. The
CC invention is useful for producing an antibody that specifically binds to
CC pancreas-derived plasminogen activator inhibitor (PAPAI) polypeptide. The
CC present sequence is human plasminogen activator inhibitor (PAI) protein.
XX
SQ Sequence 402 AA;
Query Match 100.0%; Score 2071; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSFY 60
DB 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSFY 60
QY 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
DB 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
QY 121 FVQDRLKLVQGMFPHFRFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKGV 180
DB 121 FVQDRLKLVQGMFPHFRFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKGV 180
QY 181 DQTLRLVLNLYFNGQWKTTPDSTHRRLFHKSDGSTVSPVMAQTNKKNYTFETTPD 240
DB 181 DQTLRLVLNLYFNGQWKTTPDSTHRRLFHKSDGSTVSPVMAQTNKKNYTFETTPD 240
QY 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLPK 300
DB 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKGNNTRLPRLVLPK 300
QY 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
DB 301 FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
QY 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
DB 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
RESULT 17
ABM80915
ID ABM80915 standard; protein; 402 AA.
XX
XX ABM80915;
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO2604, SEQ:2362.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX
XX
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tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.

Hom sapiens.

WO2004030615-A2.

15-APR-2004.

29-SEP-2003; 2003WO-US028547.

02-OCT-2002; 2002US-0414971P.

(GETH) GENENTECH INC.

Wu TD, Zhang Z, Zhou Y;

WPI; 2004-347921/32.

N-PSDB; ACN38690.

New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

Claim 12; SEQ ID NO 2362; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention

Query Match 100.0%; Score 2071; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHLASDFGVRVFOQAQSKDRNVFSPY 60
Db 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHLASDFGVRVFOQAQSKDRNVFSPY 60

Qy 61 GVASVLAMQLTTGGTQQQQAAMGFKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTGGTQQQQAAMGFKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120

Qy 121 FVQRDLKLVQGFMPHFRLPSTVKQDFSEVERARFTIINDVKTHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLPSTVKQDFSEVERARFTIINDVKTHTKGMISNLLGKAV 180

Qy 181 DQLTRLVLNVALYFNGQWKTPFPDSSTHRRLLFKHSDGSTSVSPVMAQTNKFNYTEFTTPD 240
Db 181 DQLTRLVLNVALYFNGQWKTPFPDSSTHRRLLFKHSDGSTSVSPVMAQTNKFNYTEFTTPD 240

Qy 241 GHYYDILELPYHGDTLSMFTAAPEYKEVPLSALTNILSAQLISHWKGNTLRLPLLLPK 300
Db 241 GHYYDILELPYHGDTLSMFTAAPEYKEVPLSALTNILSAQLISHWKGNTLRLPLLLPK 300

Qy 301 FSLTEVDLRLKPLENLGMDMFRQFQADFTSLSDQEBPLHVAQALQKVKIEVNESTGVASS 360
Db 301 FSLTEVDLRLKPLENLGMDMFRQFQADFTSLSDQEBPLHVAQALQKVKIEVNESTGVASS 360

Qy 361 STAVIVSARMAPBEIIMDRPFLFVVRHNPTGTVLFMGVNMEP 402
Db 361 STAVIVSARMAPBEIIMDRPFLFVVRHNPTGTVLFMGVNMEP 402

RESULT 18
ADP23374
ID ADP23374 standard; protein; 402 AA.
XX AC ADP23374;
XX DT 18-NOV-2004 (first entry)
XX DE PRO polypeptide SEQ ID NO:552.
XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX OS Unidentified.
XX PN WO2004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US04312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX (GETH) GENENTECH INC.
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX WPI; 2004-419628/39.
DR N-PSDB; ADP23373.
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX PS Claim 7; SEQ ID NO 552; 2940pp; English.
XX CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, an
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 402 AA;
Query Match 100.0%; Score 2071; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQSKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQSKDRNVVFSY 60
Qy 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGFMPHFRLFRSTYKQVDFSEVERARFIINDWVTKTHKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTYKQVDFSEVERARFIINDWVTKTHKGMISNLLGKAV 180
Qy 181 DQTLRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Db 181 DQTLRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Qy 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKNMTRLPRLVLPLK 300
Db 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKNMTRLPRLVLPLK 300
Qy 301 FSLETEVDLRKPLENLGTMDFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGTMDFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLPMGQVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLPMGQVMEP 402
RESULT 19
ADQ39257
ID ADQ39257 standard; protein; 402 AA.
XX
AC ADQ39257;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 920.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiact; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX

DR WPI: 2004-533949/51.
DR N-PSDB; ADQ38429.
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 920; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 402 AA;
Query Match 100.0%; Score 2071; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQSKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGESAVHPPSYVAHLASDFGVRVFOQVAQSKDRNVVFSY 60
Qy 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGFMPHFRLFRSTYKQVDFSEVERARFIINDWVTKTHKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTYKQVDFSEVERARFIINDWVTKTHKGMISNLLGKAV 180
Qy 181 DQTLRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Db 181 DQTLRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPVMAQTNKFNTEFTTPD 240
Qy 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKNMTRLPRLVLPLK 300
Db 241 GHYDILELPYHGDTLNLSMFIAPYEKEVPLSALTNILSAQLISHWKNMTRLPRLVLPLK 300
Qy 301 FSLETEVDLRKPLENLGTMDFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGTMDFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLPMGQVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLPMGQVMEP 402
RESULT 20

CC mammal. The method is useful in treating a mammal having a tumor of glial
 CC origin comprising cells that express a type A or B glial tumor antigen.
 CC This sequence represents a human tumor-associated antigenic target
 CC polypeptide.

XX
 XX
 SQ Sequence 402 AA;
 Query Match 100.0%; Score 2071; DB 9; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHILASDFGVRFQVQAQSKDRNVVFSFY 60
 Db 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHILASDFGVRFQVQAQSKDRNVVFSFY 60
 Qy 61 GVASVLAMQLTGTGGETQQOIAAMGFKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120
 Db 61 GVASVLAMQLTGTGGETQQOIAAMGFKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120
 Qy 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDKGMISNLLGKGV 180
 Db 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDKGMISNLLGKGV 180
 Qy 181 DQTLRLVLNLYFNGQWKTTPPDSSTHRRLFHKS DGS TVSPVMAQTNKFNTEFTTPD 240
 Db 181 DQTLRLVLNLYFNGQWKTTPPDSSTHRRLFHKS DGS TVSPVMAQTNKFNTEFTTPD 240
 Qy 241 GHYDILELPYHGD TSLMFIAPYEKEVPLSALTNLSAQLSHKGNNTRLPRLVL 300
 Db 241 GHYDILELPYHGD TSLMFIAPYEKEVPLSALTNLSAQLSHKGNNTRLPRLVL 300
 Qy 301 FSLETEVDLRKPLENLGMDTMRQADFTSLSDQEPHVAQALQKVIENESGTVA 360
 Db 301 FSLETEVDLRKPLENLGMDTMRQADFTSLSDQEPHVAQALQKVIENESGTVA 360
 Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTGLPMGVMEP 402
 Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTGLPMGVMEP 402

RESULT 22

AEA81039

ID AEA81039 standard; protein; 402 AA.

XX AEA81039;

XX AEA81039;

DT 08-SEP-2005 (first entry)

XX Human plasminogen activator inhibitor-1 protein SEQ ID NO:6.

DE antisense therapy; RNA interference; plasminogen activator inhibitor-1;

KW vasotropic; thrombolytic; hemostatic; vascular disease;

KW thrombocyte disorder.

XX Homo sapiens.

OS US2005148527-A1.

XX 07-JUL-2005.

XX 24-FEB-2005; 2005US-00512496.

XX 23-APR-2002; 2002US-00128706.

PR 23-APR-2003; 2003WO-US012767.

XX (ITES/) ITESCU S.

XX Itescu S;

PI WPI; 2005-478099/48.

XX N-PSDB; AEA81038, AEA81050.

XX New catalytic nucleic acid that specifically cleaves an mRNA encoding a

PT

PT plasminogen activator inhibitor-1 (PAI-1), useful for treating vascular,
 PT thrombotic or hemostatic disorders.

PS Disclosure; SEQ ID NO 6; 53pp; English.

XX The invention relates to a catalytic nucleic acid that specifically
 CC cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1).
 CC Also described: (1) a pharmaceutical composition comprising the catalytic
 CC nucleic acid, oligonucleotide, or inhibitor of PAI-1 expression, and a
 CC carrier; (2) a method of treating a cardiovascular disease in a subject;
 CC (3) a method of treating a vascular disease in a subject where the
 CC disease is treated by reducing thrombin or fibrin production; (4) a
 CC method of treating a vascular disease in a subject where the vascular
 CC disease is treated by inhibition of PAI-1 expression; (5) a method of
 CC inducing neovascularization in a heart tissue of a subject; (6) a method
 CC of inhibiting smooth muscle cell proliferation in a tissue of a subject;
 CC (7) a method of inhibiting thrombin and fibrin deposition in a heart or
 CC tissue of a subject; (8) a method of treating a subject suffering from a
 CC thrombotic disease or disorder, or hemostatic disorder where the disease
 CC or disorder is associated with elevated expression of PAI-1; and (9) a
 CC method of treating a disorder of a subject's heart involving loss of
 CC cardiomyocytes. The nucleic acid, compositions and methods are useful for
 CC treating vascular, thrombotic or hemostatic disorders. The present
 CC sequence represents human PAI-1, which is used in the exemplification of
 CC the present invention.

XX Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 9; Length 402;

Best Local Similarity 100.0%; Pred. No. 4.4e-190;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHILASDFGVRFQVQAQSKDRNVVFSFY 60

Db 1 MQMSPALTCVLGLALVFGESAVHHPPSYVAHILASDFGVRFQVQAQSKDRNVVFSFY 60

Qy 61 GVASVLAMQLTGTGGETQQOIAAMGFKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120

Db 61 GVASVLAMQLTGTGGETQQOIAAMGFKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120

Qy 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDKGMISNLLGKGV 180

Db 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDKGMISNLLGKGV 180

Qy 181 DQTLRLVLNLYFNGQWKTTPPDSSTHRRLFHKS DGS TVSPVMAQTNKFNTEFTTPD 240

Db 181 DQTLRLVLNLYFNGQWKTTPPDSSTHRRLFHKS DGS TVSPVMAQTNKFNTEFTTPD 240

Qy 241 GHYDILELPYHGD TSLMFIAPYEKEVPLSALTNLSAQLSHKGNNTRLPRLVL 300

Db 241 GHYDILELPYHGD TSLMFIAPYEKEVPLSALTNLSAQLSHKGNNTRLPRLVL 300

Qy 301 FSLETEVDLRKPLENLGMDTMRQADFTSLSDQEPHVAQALQKVIENESGTVA 360

Db 301 FSLETEVDLRKPLENLGMDTMRQADFTSLSDQEPHVAQALQKVIENESGTVA 360

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTGLPMGVMEP 402

Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTGLPMGVMEP 402

RESULT 23

AE829725

ID AE829725 standard; protein; 402 AA.

XX AE829725;

XX AE829725;

DT 06-OCT-2005 (first entry)

XX Human Ser/Cys proteinase inhibitor, member 1 SEQ ID 76.

DE Epidermal growth factor receptor; EGFR signaling; genetic marker;

KW drug screening; cancer; tumor; hyperproliferation; cytostatic;

KW

immune disorder; immunomodulator; cell proliferation; cell signaling.
Homo sapiens.
WO2005067667-A2.
28-JUL-2005.
07-JAN-2005; 2005WO-US000638.
07-JAN-2004; 2004US-0535151P.
(BRIM) BRISTOL-MYERS SQUIBB CO.
Clark EA, Ford SK, Yoganathan S, Jackson DG;
WPI; 2005-522719/53.
N-PSDB; AEB29660.
Identifying mammal that will respond therapeutically to cancer treatment
by administering epidermal growth factor receptor modulator and comparing
biomarker level such as lymphocyte antigen 75 or Cadherin 17, Li cadherin
(liver-intestine).
Claim 1; SEQ ID NO 76; 264pp; English.
The invention relates to identifying a mammal that will respond
therapeutically to a method of treating cancer by administering an
epidermal growth factor receptor (EGFR) modulator comprising measuring
level of at least one biomarker nucleic acids appearing as AEB29650-
AEB29715 and/or any of the proteins appearing as AEB29716-AEB29774 given
in the specification as Table 1. The method of identifying a mammal that
will respond therapeutically to a method of treating cancer by
administering an epidermal growth factor receptor (EGFR) modulator cited
above further comprises measuring in the mammal the level of at least one
biomarker listed above, exposing the mammal to the EGFR modulator, where a
difference in the level of the at least one biomarker measured in step
(b) compared to the level of the at least one biomarker measured in step
(a) indicates that the mammal will respond therapeutically to the method
of treating cancer. Also disclosed are EGFR receptors, nucleic acids,
antibodies, microarrays and kits for determining or predicting
susceptibility or resistance to a treatment. The method is used for
determining sensitivity in patients to allow development of
individualized genetic profiles which aid in treating diseases and
disorders based on patient response at a molecular level, including
cancers, tumors, immunological disorders, proliferative disorders and
cell signaling disorders. The present sequence is one of the EGFR
signaling-related biomarker proteins.

Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MQMSPALTCLVLGALVFGESAVHHPPSYVAHLASDFGVRVFOQVAQSKDRNVFSPY 60
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Db 61 GVASVLAMQLTGTGETQQQIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180
Qy 181 DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVPMMAQTNKFNYTEFTTPD 240
Db 181 DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVPMMAQTNKFNYTEFTTPD 240
Qy 241 GHYYDILELPHYHGDTLNLSAQLISHWKGWMTLRLPLLVLPK 300

Db 241 GHYYDILELPHYHGDTLNLSAQLISHWKGWMTLRLPLLVLPK 300
Qy 301 FSLETEVDLRKPLENLGMDTDMFRQFQADFTSLSDQBLHVAQALQVKYKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGMDTDMFRQFQADFTSLSDQBLHVAQALQVKYKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

Search completed: December 13, 2005, 15:50:16
Job time : 195 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2005, 09:01:15 ; Search time 47 Seconds
(without alignments)
707.141 Million cell updates/sec

Title: US-10-506-406-2

Perfect score: 2071

Sequence: 1 MQMSPALTCVLGLALVPE.....FVVRHNTGTVLFGQWNEP 402

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB pep:*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB pep:*
- 3: /cgn2_6/ptodata/1/iaa/H COMB pep:*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2071	100.0	402	1 US-08-315-461-7	Sequence 7, Appli
2	2071	100.0	402	2 US-08-840-204-2	Sequence 2, Appli
3	2071	100.0	402	2 US-09-026-408-3	Sequence 3, Appli
4	2071	100.0	402	2 US-09-324-494A-2	Sequence 2, Appli
5	2071	100.0	402	2 US-09-902-684-3	Sequence 3, Appli
6	2071	100.0	402	2 US-10-628-395-3	Sequence 3, Appli
7	2071	96.9	390	1 US-08-121-714-6	Sequence 6, Appli
8	2007	96.9	390	1 US-08-477-108A-6	Sequence 6, Appli
9	2007	96.9	390	1 US-08-477-112-6	Sequence 6, Appli
10	2007	96.9	390	4 PCT-US93-08322-6	Sequence 6, Appli
11	1958	94.5	379	2 US-08-840-204-3	Sequence 3, Appli
12	1958	94.5	379	2 US-09-324-494A-3	Sequence 4, Appli
13	1784	86.1	402	2 US-08-948-997-4	Sequence 4, Appli
14	1784	86.1	402	2 US-09-348-817A-4	Sequence 4, Appli
15	1784	86.1	402	2 US-09-722-292-4	Sequence 5, Appli
16	791.5	38.2	397	2 US-08-948-997-5	Sequence 5, Appli
17	791.5	38.2	397	2 US-09-348-817A-5	Sequence 5, Appli
18	791.5	38.2	397	2 US-09-722-292-5	Sequence 5, Appli
19	771.5	37.3	397	6 5187089-9	Patent No. 5187089
20	770.5	37.2	397	6 5457090-2	Patent No. 5457090
21	770.5	37.2	397	6 5495001-7	Patent No. 5495001
22	768.5	37.1	397	2 US-09-860-107-1	Sequence 1, Appli
23	765.5	37.0	397	6 5187089-10	Patent No. 5187089
24	762.5	36.8	397	6 5457090-4	Patent No. 5457090
25	762	36.8	398	6 5187089-6	Patent No. 5187089
26	760	36.7	398	6 5495001-9	Patent No. 5495001
27	759.5	36.7	397	6 5187089-2	Patent No. 5187089

28	757.5	36.6	397	6 5187089-11	Patent No. 5187089
29	756	36.5	398	6 5187089-7	Patent No. 5187089
30	750	36.2	398	6 5187089-4	Patent No. 5187089
31	748	36.1	398	6 5187089-5	Patent No. 5187089
32	656.5	31.7	360	2 US-10-037-417-67	Sequence 67, Appli
33	633	30.6	377	2 US-10-037-417-66	Sequence 66, Appli
34	620	29.9	410	2 US-09-348-817A-3	Sequence 3, Appli
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36	593	28.6	410	2 US-08-948-997-2	Sequence 2, Appli
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45	530	25.6	392	2 US-10-628-395-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-315-461-7
; Sequence 7, Application US/08315461
; Patent No. 5639726
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Daniel A.
; APPLICANT: Ginzburg, David
; APPLICANT: Shore, Joseph D.
; APPLICANT: Fay, William P.
; APPLICANT: Olson, Steven T.
; APPLICANT: Francis-Chmura, Anne-Marie
; APPLICANT: Daniel T. Bitzman
; APPLICANT: Dell Paetelli
; TITLE OF INVENTION: Peptide Mediated Enhancement Of
; TITLE OF INVENTION: Thrombolysis: Methods and Compositions
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315.461
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UMIC:006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-315-461-7
Query Match 100.0%; Score 2071; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.6e-204;

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Qy	1	MQMSPAL	TCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVFSPY	60					
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Qy	61	GVASVLA	MLQLTTTGGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI	120					
Db	61	GVASVLA	MLQLTTTGGETQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI	120					
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Db	241	GHYDII	LELPYHGDTLSMFTAAPYEKEVPLSALTNILSAQLISHWGNMTRPLRLVLPK	300					
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Db	301	FSLETEVD	LKRPLENLGWTDMFRQFQADFTSLSDQEPHLVAAQLQKVKIEVNESGSTVASS	360					
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Query Match	100.0.0%;	Score 2071;	DB 2;	Length 402;
Best Local Similarity	100.0.0%;	Pred. No. 4,6e-204;		
Matches 402;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQMSPALTCVLGLALVFGGSAVHHPPSPVVAHLASDFGVRVFQQAQASKDRNVFSPY	60	
Db	1	MQMSPALTCVLGLALVFGGSAVHHPPSPVVAHLASDFGVRVFQQAQASKDRNVFSPY	60	
Qy	61	GVASVLAMLQLTTGGETQQOIQAAMGFKIDDKGMAPALRHLYKELGMPWNKDISTTTDAI	120	
Db	61	GVASVLAMLQLTTGGETQQOIQAAMGFKIDDKGMAPALRHLYKELGMPWNKDISTTTDAI	120	
Qy	121	FVQBDLKLVOGFPHFPRFRLSRSTVKQVDFSEVERARFIINDWKTHTKGMI SNLLGKGV	180	
Db	121	FVQBDLKLVOGFPHFPRFRLSRSTVKQVDFSEVERARFIINDWKTHTKGMI SNLLGKGV	180	
Qy	181	DQLTRLVLVNALVFNGOWKTPFPDSSTHRLRFLFKHSDGSTVSPVMAQTNKFNYETFTTPD	240	
Db	181	DQLTRLVLVNALVFNGOWKTPFPDSSTHRLRFLFKHSDGSTVSPVMAQTNKFNYETFTTPD	240	
Qy	241	GHYVDILELPHYGDTLSMFTAAAPYEKEVPLSALTNLISAOIISHWKGNTRLPRLLVLPK	300	
Db	241	GHYVDILELPHYGDTLSMFTAAAPYEKEVPLSALTNLISAOIISHWKGNTRLPRLLVLPK	300	
Qy	301	PSLETEVDLRKPLNENLGMTDMFQFQADFTLSLSDQBLHVAQAOLQVKI EVNESGTVASS	360	
Db	301	PSLETEVDLRKPLNENLGMTDMFQFQADFTLSLSDQBLHVAQAOLQVKI EVNESGTVASS	360	
Qy	361	STAVIVSARMAPBEIIMDRPFLFVRHNPPTGTVLFMQVMEP	402	
Db	361	STAVIVSARMAPBEIIMDRPFLFVRHNPPTGTVLFMQVMEP	402	

RESULT 3
 US-09-026-408-3
 ; Sequence 3, Application US/09026408
 ; Patent No. 6303338
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
 ; TITLE OF INVENTION: INHIBITOR
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/026.408
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/934,011
 ; FILING DATE: 15-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/024,056
 ; FILING DATE: 16-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEEFE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.0300002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-026-408-3

Query Match 100.0%; Score 2071; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.6e-204;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
DB 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
QY 61 GVASVLAMQLTGTGGTQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
DB 61 GVASVLAMQLTGTGGTQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
QY 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180
DB 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180
QY 181 DQTLRLVLNLYFNGQWKTFFPDSSTHRLFKSDGSTSVSPMMAQTNNKFNTEFTTPD 240
DB 181 DQTLRLVLNLYFNGQWKTFFPDSSTHRLFKSDGSTSVSPMMAQTNNKFNTEFTTPD 240
QY 241 GHYYDILELPYHGDTLMSFIAAPYEKEVPLSALTNILSAQLISHWKGNNMTRLPRLLLVLPK 300
DB 241 GHYYDILELPYHGDTLMSFIAAPYEKEVPLSALTNILSAQLISHWKGNNMTRLPRLLLVLPK 300
QY 301 FSLTEVDLRKPLENLTMDMFRQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
DB 301 FSLTEVDLRKPLENLTMDMFRQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
QY 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
DB 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 4
US-09-324-494A-2
Sequence 2, Application US/09324494A
Patent No. 6489143
GENERAL INFORMATION:
APPLICANT: LAWRENCE, Daniel A
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
FILE REFERENCE: 30523/167
CURRENT APPLICATION NUMBER: US/09/324,494A
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 402
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-494A-2

Query Match 100.0%; Score 2071; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.6e-204;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
DB 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
QY 61 GVASVLAMQLTGTGGTQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
DB 61 GVASVLAMQLTGTGGTQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
QY 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180

DB 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180
QY 181 DQTLRLVLNLYFNGQWKTFFPDSSTHRLFKSDGSTSVSPMMAQTNNKFNTEFTTPD 240
DB 181 DQTLRLVLNLYFNGQWKTFFPDSSTHRLFKSDGSTSVSPMMAQTNNKFNTEFTTPD 240
QY 241 GHYYDILELPYHGDTLMSFIAAPYEKEVPLSALTNILSAQLISHWKGNNMTRLPRLLLVLPK 300
DB 241 GHYYDILELPYHGDTLMSFIAAPYEKEVPLSALTNILSAQLISHWKGNNMTRLPRLLLVLPK 300
QY 301 FSLTEVDLRKPLENLTMDMFRQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
DB 301 FSLTEVDLRKPLENLTMDMFRQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
QY 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
DB 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 5
US-09-902-684-3
Sequence 3, Application US/09902684
Patent No. 6649738
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/902,684
FILING DATE: 12-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,408
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.03000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-902-684-3

Query Match 100.0%; Score 2071; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.6e-204;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
DB 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60

Qy 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKAV 180
Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Qy 241 GHYVDILELPYHGDITLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db 241 GHYVDILELPYHGDITLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Qy 301 FSLETEVDLRKPLENLGNTDMFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLGNTDMFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 6

US-10-628-395-3
; Sequence 3, Application US/10628395
; Patent No. 6893870
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
; INHIBITOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/628,395
; FILING DATE: 29-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,408
; FILING DATE: 19-FEB-2001
; APPLICATION NUMBER: US 08/934,011
; FILING DATE: 15-AUG-1997
; APPLICATION NUMBER: US 60/024,056
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0300002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-628-395-3

Query Match 100.0%; Score 2071; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 4,6e-204;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQMSPALTCVLGLALVFGGSAVHHPPSVVAHLASDFGVRVFOQVAQAASKDRNVFSPY 60
Db 1 MQMSPALTCVLGLALVFGGSAVHHPPSVVAHLASDFGVRVFOQVAQAASKDRNVFSPY 60
Qy 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
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Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKAV 180
Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Qy 241 GHYVDILELPYHGDITLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db 241 GHYVDILELPYHGDITLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Qy 301 FSLETEVDLRKPLENLGNTDMFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLGNTDMFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 7

US-08-121-714-6
; Sequence 6, Application US/08121714
; Patent No. 5470970
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,714
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 390
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-121-714-6

Query Match
Best Local Similarity 96.9%; Score 2007; DB 1; Length 390;
Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
Qy 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDWKTHKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDWKTHKGMISNLLGKAV 180
Qy 181 DQRLRLVLNLYFNGQWKTFFPDSSTHRRLFHKSDGSTSVPMMAQTNKKNYFTFTPD 240
Db 181 DQRLRLVLNLYFNGQWKTFFPDSSTHRRLFHKSDGSTSVPMMAQTNKKNYFTFTPD 240
Qy 241 GHYDILVLPYHGDTLNMFIAAPYEKEVPLSALNLSAQILSHWKNMTRLPRLVLPK 300
Db 241 GHYDILVLPYHGDTLNMFIAAPYEKEVPLSALNLSAQILSHWKNMTRLPRLVLPK 300
Qy 301 FSLETEVDLRKPLENLGTMDFRQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGTMDFRQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPT 390
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPT 390

RESULT 8
US-08-477-108A-6
Sequence 6, Application US/08477108A
Patent No. 5801001
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
APPLICANT: Zou, Zhiqiang
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,108A
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/121,714
FILING DATE: 09/01/93

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 390
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-121-714-6

Query Match
Best Local Similarity 96.9%; Score 2007; DB 1; Length 390;
Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
Qy 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTTGGETQQOIQAAAGFKIDDGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDWKTHKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGMFPHFRSTVKQVDFSEVERARFIINDWKTHKGMISNLLGKAV 180
Qy 181 DQRLRLVLNLYFNGQWKTFFPDSSTHRRLFHKSDGSTSVPMMAQTNKKNYFTFTPD 240
Db 181 DQRLRLVLNLYFNGQWKTFFPDSSTHRRLFHKSDGSTSVPMMAQTNKKNYFTFTPD 240
Qy 241 GHYDILVLPYHGDTLNMFIAAPYEKEVPLSALNLSAQILSHWKNMTRLPRLVLPK 300
Db 241 GHYDILVLPYHGDTLNMFIAAPYEKEVPLSALNLSAQILSHWKNMTRLPRLVLPK 300
Qy 301 FSLETEVDLRKPLENLGTMDFRQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGTMDFRQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPT 390
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPT 390

RESULT 9
US-08-477-112-6
Sequence 6, Application US/08477112
Patent No. 5905023
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,112
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002003
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-477-112-6

Query Match 96.9%; Score 2007; DB 1; Length 390;
Best Local Similarity 99.7%; Pred. No. 1.6e-197;
Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCLVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVFSPY 60
Db 1 MQMSPALTCLVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVFSPY 60
Qy 61 GVASVLAMLQLTGGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTGGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRLFHKSOGSTVSPVMAQTNKFNYTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRLFHKSOGSTVSPVMAQTNKFNYTEFTTPD 240
Qy 241 GHYYDILELPHYGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLRLVLPK 300
Db 241 GHYYDILELPHYGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLRLVLPK 300
Qy 301 FSLETEVDLRKPLENLTMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLTMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNP 390
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNP 390

RESULT 10
PCT-US93-08322-6
; Sequence 6: Application PC/TUS9308322
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
```

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;
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08322
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
PCT-US93-08322-6

Query Match 96.9%; Score 2007; DB 4; Length 390;
Best Local Similarity 99.7%; Pred. No. 1.6e-197;
Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MQMSPALTCLVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVFSPY 60
Qy 61 GVASVLAMLQLTGGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTGGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRLFHKSOGSTVSPVMAQTNKFNYTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRLFHKSOGSTVSPVMAQTNKFNYTEFTTPD 240
Qy 241 GHYYDILELPHYGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLRLVLPK 300
Db 241 GHYYDILELPHYGDTLNLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLRLVLPK 300
Qy 301 FSLETEVDLRKPLENLTMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLTMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNP 390
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNP 390

RESULT 11
US-08-840-204-3
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; Sequence 3, Application US/08840204
; Patent No. 6103498
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: STEFANSSON, STEINGRIMUR P.
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
; TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,204
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 30807-20004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-840-204-3

Query Match 94.5%; Score 1958; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.7e-192;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPYGVASVLAQLTTGGTQQQIOA 60

Qy 84 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQDRLKLVQGFMPHFRLPRST 143
Db 61 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQDRLKLVQGFMPHFRLPRST 120

Qy 144 VKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 203
Db 121 VKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 180

Qy 204 DSSTHRLFHKSGDSTVSPVMAQTNKFNTEFTTPDGHYDILELPHGDTLSMFIAP 263
Db 181 DSSTHRLFHKSGDSTVSPVMAQTNKFNTEFTTPDGHYDILELPHGDTLSMFIAP 240

Qy 264 YEKEVPLSALTNILSAQLISHWKGNTLRLPLLVPKFSLETEVDLRKPLENLGMDNFR 323
Db 241 YEKEVPLSALTNILSAQLISHWKGNTLRLPLLVPKFSLETEVDLRKPLENLGMDNFR 300

Qy 324 QFQADFTSLSDQEPHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLF 383
Db 301 QFQADFTSLSDQEPHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLF 360

Qy 384 VVRHNPTGTVLPMQVMEP 402
Db 361 VVRHNPTGTVLPMQVMEP 379

RESULT 13
US-08-948-997-4
; Sequence 4, Application US/08948997
; Patent No. 6008020
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG
; APPLICANT: COLEMAN, TIM
; APPLICANT: LAWRENCE, DANIEL
; TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
; TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

RESULT 12
US-09-324-494A-3
; Sequence 3, Application US/09324494A
; Patent No. 6489143
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: STEFANSSON, STEINGRIMUR P.
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
; FILE REFERENCE: 30523/167
; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-324-494A-3

Query Match 94.5%; Score 1958; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.7e-192;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 VHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPYGVASVLAQLTTGGTQQQIOA 83
Db 1 VHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPYGVASVLAQLTTGGTQQQIOA 60

Qy 84 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQDRLKLVQGFMPHFRLPRST 143
Db 61 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQDRLKLVQGFMPHFRLPRST 120

Qy 144 VKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 203
Db 121 VKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 180

Qy 204 DSSTHRLFHKSGDSTVSPVMAQTNKFNTEFTTPDGHYDILELPHGDTLSMFIAP 263
Db 181 DSSTHRLFHKSGDSTVSPVMAQTNKFNTEFTTPDGHYDILELPHGDTLSMFIAP 240

Qy 264 YEKEVPLSALTNILSAQLISHWKGNTLRLPLLVPKFSLETEVDLRKPLENLGMDNFR 323
Db 241 YEKEVPLSALTNILSAQLISHWKGNTLRLPLLVPKFSLETEVDLRKPLENLGMDNFR 300

Qy 324 QFQADFTSLSDQEPHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLF 383
Db 301 QFQADFTSLSDQEPHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLF 360

Qy 384 VVRHNPTGTVLPMQVMEP 402
Db 361 VVRHNPTGTVLPMQVMEP 379

RESULT 13
US-08-948-997-4
; Sequence 4, Application US/08948997
; Patent No. 6008020
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG
; APPLICANT: COLEMAN, TIM
; APPLICANT: LAWRENCE, DANIEL
; TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
; TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2005, 15:46:54 ; Search time 164 Seconds
(without alignments)
1024.191 Million cell updates/sec

Title: US-10-506-406-2

Perfect score: 2071

Sequence: 1 NQSPALTCVLGLALVGE.....FVVRHNTGTVLFGQWNEP 402

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2071	100.0	402	3	US-09-902-684-3
2	2071	100.0	402	4	US-10-060-036-154
3	2071	100.0	402	4	US-10-193-656-10
4	2071	100.0	402	4	US-10-128-706-6
5	2071	100.0	402	4	US-10-170-385-235
6	2071	100.0	402	4	US-10-259-609-2
7	2071	100.0	402	4	US-10-368-995-4
8	2071	100.0	402	4	US-10-197-258-2
9	2071	100.0	402	4	US-10-231-956A-420
10	2071	100.0	402	4	US-10-628-395-3
11	2071	100.0	402	5	US-10-741-600-919
12	2071	100.0	402	5	US-10-741-600-920
13	2071	100.0	402	5	US-10-852-335A-140
14	2071	100.0	402	5	US-10-512-496-6
15	2071	100.0	402	5	US-10-506-406-2
16	2071	100.0	402	5	US-10-631-467-857
17	2071	100.0	402	6	US-11-060-291-8
18	1993	96.2	386	4	US-10-368-995-6
19	1958	94.5	379	4	US-10-259-609-3
20	1958	94.5	379	5	US-10-506-406-3
21	1784	86.1	402	3	US-09-957-485-4
22	1784	86.1	402	3	US-09-987-021-4
23	1784	86.1	402	4	US-10-368-995-2
24	1784	86.1	402	4	US-10-355-208-4
25	1784	86.1	402	4	US-10-752-041-4
26	1746	84.3	400	4	US-10-368-995-8
27	1680	81.1	402	4	US-10-128-706-16

28	1680	81.1	402	4	US-10-368-995-14	Sequence 14, Appl
29	1680	81.1	402	5	US-10-512-496-16	Sequence 16, Appl
30	1626	78.5	402	4	US-10-368-995-10	Sequence 10, Appl
31	1626	78.5	402	4	US-10-368-995-12	Sequence 12, Appl
32	1626	78.5	402	5	US-10-631-467-1575	Sequence 1575, Ap
33	796.5	38.5	397	5	US-10-631-467-1595	Sequence 1595, Ap
34	791.5	38.2	397	3	US-09-957-485-5	Sequence 5, Appl
35	791.5	38.2	397	3	US-09-987-021-5	Sequence 5, Appl
36	791.5	38.2	397	4	US-10-355-208-5	Sequence 5, Appl
37	791.5	38.2	397	4	US-10-752-041-5	Sequence 5, Appl
38	771.5	37.3	397	4	US-10-428-487-5	Sequence 5, Appl
39	770.5	37.2	397	4	US-10-170-385-297	Sequence 297, App
40	761	36.7	398	4	US-10-301-822-185	Sequence 185, App
41	761	36.7	398	4	US-10-755-889-136	Sequence 136, App
42	761	36.7	398	5	US-10-287-436A-501	Sequence 501, App
43	761	36.7	398	5	US-10-287-436A-1264	Sequence 1264, Ap
44	656.5	31.7	360	4	US-10-023-634-88	Sequence 88, Appl
45	656.5	31.7	360	4	US-10-037-417-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-902-684-3
; Sequence 3, Application US/09902684
; Patent No. US20020127640A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR INHIBITOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STRENS, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/902,684
; FILING DATE: 12-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,408
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/024,056
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0300002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-902-684-3

Query Match 100.0%; Score 2071; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Qy 61 GVASVLAMLQLTTCGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTTCGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRLESTVKQVDFSEVERARFIINDWVKTHTKGMSINLLKGAV 180
Db 121 FVQRDLKLVQGMFPHFRLESTVKQVDFSEVERARFIINDWVKTHTKGMSINLLKGAV 180
Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Qy 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLVLPLK 300
Db 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLVLPLK 300
Qy 301 FSLETEVDLRKPLENLTGMDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLTGMDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Qy 361 STAVIVSARMAPESIIIMDRPFLFVVRHNPTGTVLFMQVMEP 402
Db 361 STAVIVSARMAPESIIIMDRPFLFVVRHNPTGTVLFMQVMEP 402
RESULT 2
US-10-060-036-154
; Sequence 154, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060.036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-154
Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Qy 61 GVASVLAMLQLTTCGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTTCGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRLESTVKQVDFSEVERARFIINDWVKTHTKGMSINLLKGAV 180
Db 121 FVQRDLKLVQGMFPHFRLESTVKQVDFSEVERARFIINDWVKTHTKGMSINLLKGAV 180
Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
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Qy 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLVLPLK 300
Db 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLVLPLK 300
Qy 301 FSLETEVDLRKPLENLTGMDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLTGMDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Qy 361 STAVIVSARMAPESIIIMDRPFLFVVRHNPTGTVLFMQVMEP 402
Db 361 STAVIVSARMAPESIIIMDRPFLFVVRHNPTGTVLFMQVMEP 402
RESULT 3
US-10-193-656-10
; Sequence 10, Application US/10193656
; Publication No. US20030096733A1
; GENERAL INFORMATION:
; APPLICANT: NY, Tor
; APPLICANT: HOLMDAHL, Rikard
; APPLICANT: LI, Jinan
; TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
; FILE REFERENCE: 3810/1J577-US3
; CURRENT APPLICATION NUMBER: US/10/193,656
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/304,461
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/304,490
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,182
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P05121
; DATABASE ENTRY DATE: 1987-08-13
; RELEVANT RESIDUES: (1)..(402)
US-10-193-656-10
Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Qy 61 GVASVLAMLQLTTCGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTTCGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRLESTVKQVDFSEVERARFIINDWVKTHTKGMSINLLKGAV 180
Db 121 FVQRDLKLVQGMFPHFRLESTVKQVDFSEVERARFIINDWVKTHTKGMSINLLKGAV 180
Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNYTEFTTPD 240
Qy 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLVLPLK 300
Db 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLVLPLK 300
Qy 301 FSLETEVDLRKPLENLTGMDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLTGMDMFRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Qy 361 STAVIVSARMAPESIIIMDRPFLFVVRHNPTGTVLFMQVMEP 402
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Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGVMEP 402
|||||

RESULT 4
US-10-128-706-6
; Sequence 6, Application US/10128706
; Publication No. US20030199463A1
; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
; CURRENT APPLICATION NUMBER: US/10/128,706
; FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 402
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-128-706-6

Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQAQAKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQAQAKDRNVVFSY 60
Qy 61 GVASVLAMLOLTTCGETOOQIOAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLOLTTCGETOOQIOAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKAV 180
Qy 181 DQTLRLVLNLYFNGQWKTTPPDSTHRRLFHKSDGSTSVSPVMAQTNKFNYTEFTTPD 240
Db 181 DQTLRLVLNLYFNGQWKTTPPDSTHRRLFHKSDGSTSVSPVMAQTNKFNYTEFTTPD 240
Qy 241 GHYDILELPYHGDLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLLLVLPK 300
Db 241 GHYDILELPYHGDLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLLLVLPK 300
Qy 301 FSLETEVDLRKPLENLGMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLGMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGVMEP 402
|||||

RESULT 5
US-10-170-385-235
; Sequence 235, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Mundy, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harrie, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170,385

; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-235

Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQAQAKDRNVVFSY 60
Db 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQAQAKDRNVVFSY 60
Qy 61 GVASVLAMLOLTTCGETOOQIOAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLOLTTCGETOOQIOAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Qy 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGMFPHFRLFRSTVKQVDFSEVERARFIINDVKTHTKGMISNLLGKAV 180
Qy 181 DQTLRLVLNLYFNGQWKTTPPDSTHRRLFHKSDGSTSVSPVMAQTNKFNYTEFTTPD 240
Db 181 DQTLRLVLNLYFNGQWKTTPPDSTHRRLFHKSDGSTSVSPVMAQTNKFNYTEFTTPD 240
Qy 241 GHYDILELPYHGDLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLLLVLPK 300
Db 241 GHYDILELPYHGDLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPRLLLVLPK 300
Qy 301 FSLETEVDLRKPLENLGMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLGMDMFRQFADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGVMEP 402
|||||

RESULT 6
US-10-259-609-2
; Sequence 2, Application US/10259609
; Publication No. US20030216321A1
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, Daniel A
; APPLICANT: STEFANSON, Steingrimumur P
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES T
; FILE REFERENCE: 30523/167
; CURRENT APPLICATION NUMBER: US/10/259,609
; FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/324,494A
; FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-259-609-2

Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQAQAKDRNVVFSY 60
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Db      1  MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Qy      61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Db      61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Qy     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Db     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Qy     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Db     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Qy     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Qy     301  FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db     301  FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy     361  STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db     361  STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 7
US-10-368-995-4
; Sequence 4, Application US/10368995
; Publication No. US2003021731A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Eren, Mesut
; APPLICANT: Declerk, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
; TITLE OF INVENTION: ANIMAL
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
us-10-368-995-4

Query Match      100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Db      1  MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Qy     61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Db     61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Qy     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Db     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Qy     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Db     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Qy     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Qy     301  FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy      1  MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Db      1  MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Qy     61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Db     61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Qy     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Db     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Qy     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Db     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Qy     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Qy     301  FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
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Db      301  FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy      361  STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db      361  STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 8
US-10-197-258-2
; Sequence 2, Application US/10197258
; Publication No. US20040014190A1
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: GORLATOVA, NATALIA
; APPLICANT: CRANDALL, DAVID L.
; TITLE OF INVENTION: MUTANT PROTEINASE-INHIBITORS AND USES THEREOF
; FILE REFERENCE: 030523-0187
; CURRENT APPLICATION NUMBER: US/10/197,258
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-197-258-2

Query Match      100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Db      1  MQMSPALTCVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVFSY 60
Qy     61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Db     61  GVASVLAMLQTTGGTGTQQQIQAAAGFKIDDKGMAPALRHLYKELMGPNWKNDEISTTDAI 120
Qy     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Db     121  FVQRDLKLVQGFMPHFRLPRSTVKQVDFSEVERARFIINDWVKTHTKGMSNLLGKGV 180
Qy     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Db     181  DQLTRLVLVNALYFNGQWKTFPPDSSTHRRLFHKSDGSTSVSPVMAQTNKNFYTEFTTPD 240
Qy     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db     241  GHYYDILELPHYGDTLNMFIAAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Qy     301  FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db     301  FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Qy     361  STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db     361  STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 9
US-10-231-956A-420
; Sequence 420, Application US/10231956A
; Publication No. US2004005323A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Xu, Weiduan
; APPLICANT: Bogenberger, Jakob
; APPLICANT: Holland, Sacha
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Modulators of Angiogenesis
; FILE REFERENCE: 021044-00410005
```



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; CURRENT APPLICATION NUMBER: US/10/231.956A
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 420
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-956A-420

Query Match      100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOOVAQAKDRNVVSPY 60
Db 1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOOVAQAKDRNVVSPY 60

Qy 61 GVASVLAMQLTGTGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTGTGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120

Qy 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180

Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNTEFTTPD 240

Qy 241 GHYVDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db 241 GHYVDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300

Qy 301 FSLETEVDLRKPLENLGTMDFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGTMDFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 10
US-10-628-395-3
; Sequence 3, Application US/10628395
; Publication No. US20040086978A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR INHIBITOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/628,395
; FILING DATE: 29-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,408
; FILING DATE: 19-FEB-2001
; APPLICATION NUMBER: US 08/934,011
; FILING DATE: 15-AUG-1997

; CURRENT APPLICATION NUMBER: US/10/231.956A
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 420
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-956A-420

Query Match      100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOOVAQAKDRNVVSPY 60
Db 1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOOVAQAKDRNVVSPY 60

Qy 61 GVASVLAMQLTGTGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTGTGETQQOIQAAAGFKIDDKGAPALRHLYKELMGPNKDEISTTDAI 120

Qy 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLGKAV 180

Qy 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNTEFTTPD 240
Db 181 DQTRLVLVNALYFNGQWKTFFPDSSTHRRLFHKSDGSTSVSPMMAQTNKFNTEFTTPD 240

Qy 241 GHYVDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300
Db 241 GHYVDILELPYHGDTLSMFIAPYEKEVPLSALTNILSAQLISHWKGNTLRLPLLVLPK 300

Qy 301 FSLETEVDLRKPLENLGTMDFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEVDLRKPLENLGTMDFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVA 360

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 11
US-10-741-600-919
; Sequence 919, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 919
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-919

Query Match      100.0%; Score 2071; DB 5; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
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; CURRENT APPLICATION NUMBER: US/10/512,496
; CURRENT FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 402
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-512-496-6

Query Match      100.0%; Score 2071; DB 5; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVPSY 60
Db      1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVPSY 60

Qy      61 GVASVLAMLQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
Db      61 GVASVLAMLQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120

Qy      121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDVKTKHGMISNLLGKGV 180
Db      121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDVKTKHGMISNLLGKGV 180

Qy      181 DQTLRLVLNVALYFNGQWKTFFPDSSSTRRLFKHSDGSTSVSPMMAQTNKFNTEFTTPD 240
Db      181 DQTLRLVLNVALYFNGQWKTFFPDSSSTRRLFKHSDGSTSVSPMMAQTNKFNTEFTTPD 240

Qy      241 GHYDILLELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLLLVLPK 300
Db      241 GHYDILLELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLLLVLPK 300

Qy      301 FSLTEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
Db      301 FSLTEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360

Qy      361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402
Db      361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402

RESULT 15
US-10-506-406-2
; Sequence 2, Application US/10506406
; Publication No. US20050158295A1
; GENERAL INFORMATION:
; APPLICANT: Swiercz, Rafal.
; APPLICANT: Selman, Steven
; APPLICANT: Jankun, Jerzy
; APPLICANT: Chorostowska-Wynimko, Joanna
; APPLICANT: Skrzypczak-Jankun, Ewa
; TITLE OF INVENTION: MODIFIED PLASMINOGEN ACTIVATOR INHIBITOR
; TITLE OF INVENTION: TYPE-1 AND METHODS BASED THEREON
; FILE REFERENCE: 9471-011-999
; CURRENT APPLICATION NUMBER: US/10/506,406
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: PCT/US03/06679
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,670
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human PAI-1 amino acid sequence, including signal peptide
US-10-506-406-2

Query Match      100.0%; Score 2071; DB 5; Length 402;
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Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVPSY 60
Db      1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVPSY 60

Qy      61 GVASVLAMLQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
Db      61 GVASVLAMLQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120

Qy      121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDVKTKHGMISNLLGKGV 180
Db      121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDVKTKHGMISNLLGKGV 180

Qy      181 DQTLRLVLNVALYFNGQWKTFFPDSSSTRRLFKHSDGSTSVSPMMAQTNKFNTEFTTPD 240
Db      181 DQTLRLVLNVALYFNGQWKTFFPDSSSTRRLFKHSDGSTSVSPMMAQTNKFNTEFTTPD 240

Qy      241 GHYDILLELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLLLVLPK 300
Db      241 GHYDILLELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLLLVLPK 300

Qy      301 FSLTEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360
Db      301 FSLTEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHLVAQALQKVKIEVNESGTVA 360

Qy      361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402
Db      361 STAVIVSARMAPEIIMDRPFLFVVRHNPTGTVLFMQGVMEP 402

RESULT 16
US-10-631-467-857
; Sequence 857, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 857
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-857

Query Match      100.0%; Score 2071; DB 5; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVPSY 60
Db      1 MQMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVPSY 60

Qy      61 GVASVLAMLQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
Db      61 GVASVLAMLQLTTGGTQQOIQAAAGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120

Qy      121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDVKTKHGMISNLLGKGV 180
Db      121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDVKTKHGMISNLLGKGV 180

Qy      181 DQTLRLVLNVALYFNGQWKTFFPDSSSTRRLFKHSDGSTSVSPMMAQTNKFNTEFTTPD 240
Db      181 DQTLRLVLNVALYFNGQWKTFFPDSSSTRRLFKHSDGSTSVSPMMAQTNKFNTEFTTPD 240
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Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 VHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPYGVASVLAMLQLTTGGTQQQIOA 83
Db 1 VHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPYGVASVLAMLQLTTGGTQQQIOA 60

Qy 84 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQRDLKLVQGFMPHFRFLFRST 143
Db 61 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQRDLKLVQGFMPHFRFLFRST 120

Qy 144 VKQVDFSEVERARFIINDWVKTHTKGMI-SNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 203
Db 121 VKQVDFSEVERARFIINDWVKTHTKGMI-SNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 180

Qy 204 DSSTHRRLLFKHSDGTSVSPVMAQTNKFNVTFTTPDGHYDILELPHYHGTLSMFTAAP 263
Db 181 DSSTHRRLLFKHSDGTSVSPVMAQTNKFNVTFTTPDGHYDILELPHYHGTLSMFTAAP 240

Qy 264 YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMDMFR 323
Db 241 YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMDMFR 300

Qy 324 QFQADFTSLSDQEPHVAQALQKVKIEVNSGTVASSSTAVIVSARMAPEEIIIMDRPFLF 383
Db 301 QFQADFTSLSDQEPHVAQALQKVKIEVNSGTVASSSTAVIVSARMAPEEIIIMDRPFLF 360

Qy 384 VVRHNPTGTVLPMQVMEP 402
Db 361 VVRHNPTGTVLPMQVMEP 379

RESULT 20

US-10-506-406-3
; Sequence 3, Application US/10506406
; Publication No. US20050158295A1
; GENERAL INFORMATION:
; APPLICANT: Swiercz, Rafal
; APPLICANT: Selman, Steven
; APPLICANT: Jankun, Jerzy
; APPLICANT: Chorostowska-Wynimko, Joanna
; APPLICANT: Skrzypczak-Jankun, Ewa
; TITLE OF INVENTION: MODIFIED PLASMINOGEN ACTIVATOR INHIBITOR
; TITLE OF INVENTION: TYPE-1 AND METHODS BASED THEREON
; FILE REFERENCE: 9471-011-399
; CURRENT APPLICATION NUMBER: US/10/506,406
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: PCT/US03/06679
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,670
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human PAI-1 mature amino acid sequence

US-10-506-406-3

Query Match 94.5%; Score 1958; DB 5; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-179;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 VHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPYGVASVLAMLQLTTGGTQQQIOA 83
Db 1 VHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPYGVASVLAMLQLTTGGTQQQIOA 60

Qy 84 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQRDLKLVQGFMPHFRFLFRST 143
Db 61 AMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAIFVQRDLKLVQGFMPHFRFLFRST 120

Qy 144 VKQVDFSEVERARFIINDWVKTHTKGMI-SNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 203

Db 121 VKQVDFSEVERARFIINDWVKTHTKGMI-SNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 180

Qy 204 DSSTHRRLLFKHSDGTSVSPVMAQTNKFNVTFTTPDGHYDILELPHYHGTLSMFTAAP 263
Db 181 DSSTHRRLLFKHSDGTSVSPVMAQTNKFNVTFTTPDGHYDILELPHYHGTLSMFTAAP 240

Qy 264 YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMDMFR 323
Db 241 YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMDMFR 300

Qy 324 QFQADFTSLSDQEPHVAQALQKVKIEVNSGTVASSSTAVIVSARMAPEEIIIMDRPFLF 383
Db 301 QFQADFTSLSDQEPHVAQALQKVKIEVNSGTVASSSTAVIVSARMAPEEIIIMDRPFLF 360

Qy 384 VVRHNPTGTVLPMQVMEP 402
Db 361 VVRHNPTGTVLPMQVMEP 379

RESULT 21

US-09-957-485-4
; Sequence 4, Application US/09957485
; Patent No. US20020143165A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
; TITLE OF INVENTION: Activator
; FILE REFERENCE: PF336P1
; CURRENT APPLICATION NUMBER: US/09/957,485
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 09/521,664
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US 60/123,704
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Bos taurus
; OTHER INFORMATION: US-09-957-485-4

Query Match 86.1%; Score 1784; DB 3; Length 402;
Best Local Similarity 85.3%; Pred. No. 1.2e-162;
Matches 343; Conservative 29; Mismatches 30; Indels 0; Gaps 0;

Qy 1 NQMSPALTCLVLGLALVFGESAVHHPPSYVAHLASDFGVRVFOQVAQASKDRNVVSPY 60
Db 1 MRMSVPACALGLALIFGEGSAGYQPSAASALATDFGVKVFQVVRASKDRNVVSPY 60

Qy 61 GVASVLAMLQLTTGGTQQQIOAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTTGGTQQQIOAAMGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120

Qy 121 FVQRDLKLVQGFMPHFRFLFRSTVKQVDFSEVERARFIINDWVKTHTKGMI-SNLLGKGA 180
Db 121 FVQRDLKLVQGFMPHFRFLFRSTVKQVDFSEVERARFIINDWVKTHTKGMI-SNLLGKGA 180

Qy 181 DQLTRLVLVNALYFNGQWKTPFPDSSSTHRRLLFKHSDGTSVSPVMAQTNKFNVTFTTPD 240
Db 181 DQLTRLVLVNALYFNGQWKTPFPDSSSTHRRLLFKHSDGTSVSPVMAQTNKFNVTFTTPD 240

Qy 241 GHYDILELPHYHGTLSMFTAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
Db 241 GHYDILELPHYHGTLSMFTAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300

Qy 301 FSLETEVDLRKPLENLGMDMFRQFQADFTSLSDQEPHVAQALQKVKIEVNSGTVASS 360
Db 301 FSLETEVDLRKPLENLGMDMFRQFQADFTSLSDQEPHVAQALQKVKIEVNSGTVASS 360

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLPMQVMEP 402
Db 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLPMQVMEP 402

Db 361 STALVVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 22

US-09-987-021-4
; Sequence 4, Application US/09987021
; Patent No. US20020165147A1
; GENERAL INFORMATION:
; APPLICANT: Yepez, et al.
; TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator
; FILE REFERENCE: PF336P2
; CURRENT APPLICATION NUMBER: US/09/987,021
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/957,485
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/722,292
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/247,971
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 09/521,664
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/348,817
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/123,704
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 08/948,997
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/028,117
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-987-021-4

Query Match 86.1%; Score 1784; DB 3; Length 402;
Best Local Similarity 85.3%; Pred. No. 1.2e-162;
Matches 343; Conservative 29; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MOMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAASKDRNVVFSY 60
Db 1 MRMSPVFACIALGLALIFGEGSASYQPSAASLATDFGVKVFQVVRASKDRNVVFSY 60

Qy 61 GVASVLAMLQLTTGGTQQQIQAAAMGFKIDDKGMAPALRHLKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTTGGTQQQIQEAMQFKIEKGMAPAFHRLYKELMGPNKDEISTADAI 120

Qy 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLKGAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLKGAV 180

Qy 181 DQTLRLVLNVALYFNGQWKTPFPDSSTHRLRFLHKS DGSSTVSPVMAQTNKFNYTEFTTPD 240
Db 181 DQTLRLVLNVALYFNGQWKMPFPESNTHRLRFLHKS DGSSTVSPVMAQTNKFNYTEFTTPD 240

Qy 241 GHYYDILELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKNMTRLPRLLLVLPK 300
Db 241 GRYYDILELPYHGNTLSMLIAAPAEYKEVPLSALTSILDABELISQWKGNMTRLPRLLLVLPK 300

Qy 301 FSLETEVDLRKPLENLGMDTDFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEIDLRRLPLENLGMDTDFRPSQADFSSDQEFLYVSQALQKVKIEVNESGTIASS 360

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STALVVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 23
US-10-368-995-2
; Sequence 2, Application US/10368995

; Publication No. US20030217371A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Bren, Mesut
; APPLICANT: Declerk, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
; TITLE OF INVENTION: ANIMAL
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Cow
US-10-368-995-2

Query Match 86.1%; Score 1784; DB 4; Length 402;
Best Local Similarity 85.3%; Pred. No. 1.2e-162;
Matches 343; Conservative 29; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MOMSPALTCVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFOQVAQAASKDRNVVFSY 60
Db 1 MRMSPVFACIALGLALIFGEGSASYQPSAASLATDFGVKVFQVVRASKDRNVVFSY 60

Qy 61 GVASVLAMLQLTTGGTQQQIQAAAMGFKIDDKGMAPALRHLKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMLQLTTGGTQQQIQEAMQFKIEKGMAPAFHRLYKELMGPNKDEISTADAI 120

Qy 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLKGAV 180
Db 121 FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARFIINDWVTKHTKGMISNLLKGAV 180

Qy 181 DQTLRLVLNVALYFNGQWKTPFPDSSTHRLRFLHKS DGSSTVSPVMAQTNKFNYTEFTTPD 240
Db 181 DQTLRLVLNVALYFNGQWKMPFPESNTHRLRFLHKS DGSSTVSPVMAQTNKFNYTEFTTPD 240

Qy 241 GHYYDILELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKNMTRLPRLLLVLPK 300
Db 241 GRYYDILELPYHGNTLSMLIAAPAEYKEVPLSALTSILDABELISQWKGNMTRLPRLLLVLPK 300

Qy 301 FSLETEVDLRKPLENLGMDTDFRQFQADFTSLSDQEPHVAQALQKVKIEVNESGTVASS 360
Db 301 FSLETEIDLRRLPLENLGMDTDFRPSQADFSSDQEFLYVSQALQKVKIEVNESGTIASS 360

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STALVVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

Search completed: December 13, 2005, 15:53:12
Job time : 172 secs

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OM protein - protein search, using sw model

Run on: December 13, 2005, 09:13:06 ; Search time 12 seconds

(without alignments)
187.078 Million cell updates/sec

Title: US-10-506-406-2

Perfect score: 2071

Sequence: 1 MQMSPALTCVLGLALVFE.....FVVRHNPFTGTVLFMGQWNEP 402

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2071	100.0	402	US-10-821-234-1581	Sequence 1581, Ap
2	761	36.7	398	US-10-821-234-1488	Sequence 1488, Ap
3	761	36.7	398	US-11-186-284-185	Sequence 185, App
4	461	22.3	423	US-10-821-234-900	Sequence 900, App
5	441	21.3	391	US-10-623-155-110	Sequence 110, App
6	440	21.2	425	US-11-096-276-2	Sequence 2, Appli
7	438.5	21.2	400	US-10-623-155-112	Sequence 112, App
8	436.5	21.1	417	US-11-147-047-39	Sequence 39, Appl
9	398.5	19.2	444	US-11-071-580-1	Sequence 1, Appli
10	394.5	19.0	444	US-10-131-826A-498	Sequence 498, App
11	312	15.1	500	US-10-821-234-1458	Sequence 1458, App
12	308.5	14.9	418	US-11-186-284-187	Sequence 187, App
13	305	14.7	418	US-10-821-234-1331	Sequence 1331, App
14	304	14.7	418	US-11-077-716-2	Sequence 2, Appli
15	219	10.6	362	US-11-010-874-18	Sequence 18, Appl
16	202.5	9.8	366	US-10-215-245A-2	Sequence 2, Appli
17	92.5	4.5	347	US-10-793-626-3326	Sequence 3326, Ap
18	87.5	4.2	530	US-10-131-826A-130	Sequence 130, App
19	87	4.2	1034	US-10-392-234A-30	Sequence 30, Appl
20	86	4.2	484	US-10-793-626-2498	Sequence 2498, Ap
21	86	4.2	1065	US-10-793-626-1212	Sequence 1212, Ap
22	83.5	4.0	448	US-10-793-626-1728	Sequence 1728, Ap
23	81.5	3.9	717	US-10-793-626-3022	Sequence 3022, Ap
24	81.5	3.9	952	US-10-821-234-1557	Sequence 1557, Ap
25	81.5	3.9	952	US-11-057-058-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1

US-10-821-234-1581
; Sequence 1581, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt:seq_genes Version 1.0
; SEQ ID NO 1581
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1581

Query Match	100.0%	Score 2071;	DB 6;	Length 402;
Best Local Similarity	100.0%	Pred. No. 7.3e-179;		
Matches 402;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQMSPALTCVLGLALVFE	GSVAHHPPSYVAH	LAASDFGVRVFOQAQSKDRNVFESPY 60
Db	1	MQMSPALTCVLGLALVFE	GSVAHHPPSYVAH	LAASDFGVRVFOQAQSKDRNVFESPY 60
Qy	61	GVASVLA	MLQLTGTG	GTGQQQAAMGPKIDDKGMALRHLYKELGMPNKDEISTTDAI 120
Db	61	GVASVLA	MLQLTGTG	GTGQQQAAMGPKIDDKGMALRHLYKELGMPNKDEISTTDAI 120
Qy	121	FVQRDLKLVQGFMPHF	FRFRSTVKQVDFSEVERARFI	INDVWKTHTKGMISNLLGKGAV 180
Db	121	FVQRDLKLVQGFMPHF	FRFRSTVKQVDFSEVERARFI	INDVWKTHTKGMISNLLGKGAV 180
Qy	181	DQLTRLVN	ALYFNGQWKT	PPDSSTHRLPHKSDGSTSVSPMMAQTNKFNFTFTTDP 240
Db	181	DQLTRLVN	ALYFNGQWKT	PPDSSTHRLPHKSDGSTSVSPMMAQTNKFNFTFTTDP 240
Qy	241	GHYDILEL	PHYHGD	TLSMFIAAPYKEVPLSALTNILSAQLISHWKGNNTRLPRLVLVLPK 300
Db	241	GHYDILEL	PHYHGD	TLSMFIAAPYKEVPLSALTNILSAQLISHWKGNNTRLPRLVLVLPK 300
Qy	301	FSLETEVD	LURKPLEN	LGMTDMFRQFADFTSLSDQEPHLHVAQALQVKIEVNESGTVASS 360

Db	301	FSLETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPFLHVAQALQVKIVNESGTVASS	360
Qy	361	STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQWMEP	402
Db	361	STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQWMEP	402

```

RESULT 2
US-10-821-234-1488
; Sequence 1488, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt-seq_genes Version 1.0
; SEQ ID NO 1488
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1488

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Query Match	36.7%	Score 761;	DB 6;	Length 398;
Best Local Similarity	41.3%;	Pred. No. 3.5e-61;		
Matches 157; Conservative	77;	Mismatches 142;	Indels 4;	Gaps 3;

Qy	25	HHPPSYVAHLASDFGRVFQOQAOKSDRNNVFSPYGVASVLAMLQLTGTGTOQQIQAA	84
Db	21	HFNPLSLEECSNTGIGVFQIQVKSRRPHDNIVISPHGIASVLGMLQCADGRTKKKQAMV	80
Qy	85	MGFKIDDKGMAPALRHLYKELMGPMWNKDEISTTDAIFVQRDLKVLQGMGPHFFLFRSTV	144
Db	81	MRYGVN--GVGKILUKINKAIVASKKNKDITVNAVAVFQNAASEIEVPFVTRKDVQCEV	138
Qy	145	KQYDFSEVERARFTINDQVTKTHTKGMLSNLLGKAVD-QLTRLVLVNALYENGQWKTPEP	203
Db	139	RNVNFEDPASACDSINAVQNKETRDMINDLLSPDLIDGLVTRLVLVNAVVFVGLWUKGRQV	198
Qy	204	DSSTHRLPHFKSDGSTSVSPMMAQTNKFNTEFTTPDGHYYDILDELPHYGDTLMSFTAAP	263
Db	199	PENTKRTFVAADCKSQVPMPLAQLSVFCGSGTSAPNDLWTFNFIELPYHGESISMLIALP	258
Qy	264	YEKEVPLSALTNILSAQLISHWKGNNTRLPALLVLPKFSLETEVDLRKPLENLGWTDMFR	323
Db	259	TESSTPLSAIPHISTITKIDSIMVPKRVQVILPKFTVAQAQDLKEPLKVLGITDMFD	318
Qy	324	QFOADFTSL--SDQPLHVAQALQVKIEVNESGTVASGSSTAVISASMAPEEIIIMDRPFL	382
Db	319	SSKANFAKITGSENLHVSHILOKAKIEVSEDDGTAKASNAATAILIARSSPPWFIVDRPFL	378
Qy	383	FVVRHNPTGTVLFMGQVMEP	402
Db	379	FFIRHNPTGAVLFMGQINKP	398

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RESULT 4
US-10-821-234-900
; Sequence 900, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diag
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/82
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,

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; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 900
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-900

Query Match      22.3%; Score 461; DB 6; Length 423;
Best Local Similarity 28.8%; Pred. No. 3.4e-34;
Matches 119; Conservative 76; Mismatches 163; Indels 56; Gaps 9;

QY 38 FGVRVFOQAQAKDRNVVFPYGVASVLAMQLTGTGTOOQQAAMGF-----87
DB 19 FALNLFKHLAKASPTQNLFLSPWSISSTMVYMGSRGSTDQMAKVLQFNEVGANAVTP 78
QY 88 -----KIDDKGMAP-----ALRHLKELMGPNKDEISTDAIF 121
DB 79 MTPENPTSCGFQWQIQKGSYDAILQAQAADKIHSFSLSSAINASTGNLLESVNKL 138
QY 122 VQDRLKLVQGFMPHFRLFRSTVKQVDFSE--VERARFIINDVVKTHTKGMISNLLGKAV 180
DB 139 GEKSASPREYIRLCQKYVSEPOAVDFLECAEARKKIYSWVKTTQTKGKIPNLLPEGSV 198
QY 181 DQTLRLVLNLYFNGQKTKTPDPDSSTRRLPHFKSDGTSVSPVMAQTNKFNTEFTTPD 240
DB 199 DQDTRMLVNAVYFKGKTKTPPEKKNGLYFPRVNSAORTVPQMMYLREKLN-----251
QY 241 GHYD-----ILELPHVGHDTLSMFIAAPYE---KEVPLSALTNILSAQLISHW--KGNMTR 291
DB 252 GYIEDLKAQILELPVAGD--VSNFLLPDEIADVSTGLELSEIYDKLNKTKSKKVAE 310
QY 292 LPRLLVLPKFSLETEVDLRKPLENLGMDTMRFOADFTSLSDQBLPHVAQALOKVKIEV 351
DB 311 DEVEVYIQFLEEHVELRSILRSGMEDAFNKGRAFSGMGRNDLFLSEVHFQAMVDV 370
QY 352 NEGTVASSTAVISARM--APEIIMDRPFLFVRHNPCTGLVFMQVMEP 402
DB 371 NEEGTEAAGTGVMTGRTGHGGPQFVADHPFLFLIMHKITNCILFFGFRSSP 423

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RESULT 5
US-10-623-155-110
; Sequence 110, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-623-155-110

Query Match      21.3%; Score 441; DB 6; Length 391;
Best Local Similarity 27.4%; Pred. No. 1.9e-32;
Matches 107; Conservative 92; Mismatches 165; Indels 26; Gaps 8;

QY 34 LASDFGVRVFOQAQAKDRNVVFPYGVASVLAMQLTGTGTOOQIQ-----AA 84
DB 7 VSTRLGFDLFKEL--KKTNDGNIFPSVIGILTAIMGVLLGTRGATASQLSEVFHSEKETKS 65
QY 85 MGEFKIDDKGNAPALRHLK-----ELMGPNKDEISTDAIFVQDRLKLVQGFMPHF 137

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DB 66 SRIKAEKEVIENTEAVHQFQKFLTEISKLTNDYELNITNRLFGKTYLFLQKLYDVE 125
QY 138 RLFRSTVKQVDF--SEVERARFIINDVVKTHTKGMISNLLGKAVDQDLTRLVLNLYFNG 196
DB 126 KYHASLEPVDFVNADESRRKINSWVESKIKDLFPDGSISSTKLVLNVMVYFKG 185
QY 197 QWKTFFPDSSTRRLPHFKSDGTSVSPVMAQTNKFNTEFTTPDGHYDILELPHVGHDTL 256
DB 186 QWDRFCKENTKSEKFWMNKSTKSQVMTQSHFS--FTFLEDLQAKILGIPYKNDL 242
QY 257 SMFIAAPYEKEVPLSALTNILSAQLISHW--KGNMTRPLRLVLPKFSLETEVDLRKPLE 314
DB 243 SMFVLLDNID-D-GLKIIDKISPEKLVEMTSPGHMEERKYNLHLPREFEVDSYDLEAVLA 301
QY 315 NLGMDTMRFOADFTSLSDQBLPHVAQALOKVKIEVNESGTAVSSSTAVISARM--372
DB 302 AMGMDAFSEHKADYSQSSGSLYAKQFLHSSFVAVTEGTEAAATGFTVTSAPGH 361
QY 373 BEIIMDRPFLFVRHNPCTGLVFMQVMEP 402
DB 362 ENVHCNHPFLFFIRHNESNLSILFFGFRSSP 391

RESULT 6
US-11-096-276-2
; Sequence 2, Application US/11096276
; Publication No. US20050260726A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Protease Inhibitor and Polynucleotides Encoding the s
; FILE REFERENCE: LEX-0283-USA
; CURRENT APPLICATION NUMBER: US/11/096,276
; CURRENT FILING DATE: 2005-03-31
; PRIOR FILING DATE: US/10/419,277
; PRIOR FILING DATE: 2003-04-17
; PRIOR FILING DATE: US/10/024,427
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: US 60/256,287
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: homo sapiens
; US-11-096-276-2

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Query Match      21.2%; Score 440; DB 7; Length 425;
Best Local Similarity 26.2%; Pred. No. 2.6e-32;
Matches 111; Conservative 89; Mismatches 149; Indels 74; Gaps 10;

QY 42 VFOQAQAKDRNVVFPYGVASVLAMQLTGTGTOOQQAAMGF-----KIDDKGMAPA 97
DB 15 LFQEGIKDDRHKNIFFSLSLAALGVRLGARSADSAHQIDEVLHFNFSQNESKEPDPC 74
QY 98 LRHLKELM-----GPNWKDE-----IST 116
DB 75 LKSNKQKVLADSLLEGQKKTTEPLDQAGSLNNSGLVSCYFGQLSLKLDRIKTYTLSI 134
QY 117 TDAIFVQDRLKLVQGFMPHFRLFRSTVKQVDFSE--VERARFIINDVVKTHTKGMISNLL 175
DB 135 ANRLYGEQEFPCQBYLQGVQFYHTTIESVDVDFQKNPKSROEINFVWECQSGKIKELF 194
QY 176 GKGAVDQTLRLVLNLYFNGQKTKTPDPDSSTRRLPHFKSDGTSVSPVMAQTNKFNTE 235
DB 195 SKDAINAETVLVLNAVYFKAKWETVFD-----HE---NTVDAPCLNANENKSVK 242
QY 236 FTTPDGHY-----VDILELPHVGHDTLSMFIAAPYEKEVPLSALTNI---LSQLLS 283
DB 243 MMTQKGLYRIGRIEIEVKAQILEMRYTKGKLSMFLVLLPSHSLKGLSELERKITVERKV 302

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Qy 284 HWKG--NWTRLPRLVLKPKESLSETEVDLRKPLENLGMDTMRQFQADFTSLSDQEPHVA 341
Db 303 AWSSENNSSESVLSPFRFLESDYDNLQDMGIIDFDETRADLTGSPSPNLYLS 362
Qy 342 QALQKVIEVNESGTAVSSSTAVIVSARMAPE--EIIIMDRPFLFVVRHNPPTGTVLFMGOV 399
Db 363 KIIHKTFEVDENGTAQAATGAVVSESLRSWSWFEFNNHFFLPIRHNKTQTLIFYGRV 422
Qy 400 MEP 402
Db 423 CSP 425

RESULT 7
US-10-623-155-112
; Sequence 112, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623.155
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-112

Query Match 21.2%; Score 438.5; DB 6; Length 400;
Best Local Similarity 27.1%; Pred. No. 3.3e-32;
Matches 108; Conservative 91; Mismatches 165; Indels 35; Gaps 8;

Qy 34 LASDFGVRFVFOQAQSKDRNVFSPYGVASVLAMQLTTGSETQQQIQ-----82
Db 7 VSTRLGDFLPEL-KKTNDGNIFFSPVIGLTAIGVLLGTGATASQLEEVFHSKETS 65
Qy 83 -----AAMGFKIDD-KGMAPALRHLKELMGPNKDEISTTDAIFVORDKL 128
Db 66 SRIKAEKEVVRKAEKGEIENEAHVQFQKFLTEISKLTNDYELNITNRLFGKTYLF 125
Qy 129 VQGMPPHFRFRSTVQKQDF-SEVERARFTINDWVKTHTKGMISNLLGKAVDQLTRLV 187
Db 126 LQKYLVDVEKYHSLPEVDFVNADESRRKINSWESKTEKIKDLFPDGSISSTKL 185
Qy 188 LVNALYFNGQWKTPFPDSSTHRRLFHKS DGSSTVSPVMAQTNKFNTEFTTPDGHYYDIL 247
Db 186 LVNMVYFKGQWDREKFKTEKEEFMKNKTSKSVQMTQSHSFS---FTFLEDLQAKIL 242
Qy 248 ELPHGDTLSMFIAPAEKEVPLSALTNLISQAULSHW--KGNTRLPRLVLVLPKFSLET 305
Db 243 GIPYKNNDLSMFLVLPNDID-GLEKIIDKISPEKLVEMTSPGHMEERKVNHLHLPREFVED 301
Qy 306 EVDLRKPLENLGMDTMRQFQADFTSLSDQEPHVAQALQVKIEVNESGTAVIVSARMAPE 365
Db 302 SYDLEAVLAAMGMDAFASEHKADYSGHSSGGLYAQKFLHSSFVAVTEBTEAANAATGIG 361
Qy 366 VSARMAP--EIIIMDRPFLFVVRHNPPTGTVLFMGOVMEP 402
Db 362 FTVTSAPGHENHVCNHPFLPIRHNESNLSLFFGRFSSP 400

RESULT 8
US-11-147-047-39
; Sequence 39, Application US/11147047
; Publication No. US2005026068A1
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; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147.047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221.097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-39

Query Match 21.1%; Score 436.5; DB 7; Length 417;
Best Local Similarity 28.7%; Pred. No. 5.3e-32;
Matches 111; Conservative 88; Mismatches 165; Indels 23; Gaps 9;

Qy 27 PPSVVAHLASDFGVRFVFOQAQSKDRNVFSPYGVASVLAMQLTTGSETQQQIQAAAMG 86
Db 40 PASQVYSLNTDFAFRLYRRLVLETPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLG 99
Qy 87 FKI---DDKGMAPALRHLKELMGPNKDEISTTDAIFVORDKLIVQGFPHFRFLRST 143
Db 100 FNLHTPESAIHQFGHVLVSLTPVPSKDLTKMGSAFLVKELQQLQANFLGNVKRLYEAE 159
Qy 144 VKQVDFSEVERARFTINDWVKTHTKGMISNLLGKAVDQLTRLVLNVALYFNGQWKTPFP 203
Db 160 VFSTDFSNPSIAQARINSHVKKTKQKVDII--QGLDILTANVLVNHIFFKAKWKPFFH 217
Qy 204 DSSTHRL--FKHSDGSTSVSPVMAQTNKFN---TEFTTPDGHYYDILELPHYHGDLSMF 259
Db 218 PEVTRKNFPPLVGEQVTVHVPMMHQEQPAFGVDVTELNC-----FVLQMDYKGDVAFF 271
Qy 260 IAAPYEKEVPLSALTNLISQAULSHWKGNTRLPRLVLVLPKFSLETVDLRKPLENLGMT 319
Db 272 VLPSKKGK--MRQLEQALSARTLRKWSHSLQKRWIEVFIPRFSISASYNLETILPKNGIQ 328
Qy 320 DMFRQFQADFTSLSDQEPHVAQALQVKIEVNESGT--VASSTAVIVSARMAPE--EI 375
Db 329 NVFDK--NADPSGAKRDSQVSKATHKAVLDVSEEGTEATAATTTKFIVRSKOGPSYFTV 387
Qy 376 IMDRPFLFVVRHNPPTGTVLFMGOVMEP 402
Db 388 SPNRTFLMITNKATDGIILFLGKVENP 414

RESULT 9
US-11-071-580-1
; Sequence 1, Application US/11071580
; Publication No. US20050260708A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: LAL, Preeti
```



```
; Sequence 1458, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1458
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1458

Query Match      15.1%; Score 312; DB 6; Length 500;
Best Local Similarity 26.3%; Pred. No. 1.1e-20;
Matches 107; Conservative 74; Mismatches 162; Indels 64; Gaps 14;

Qy 11 VLGALVPGEGSAVHHPPSYVAHLASDFGVRFQOQAQASK-DRNVVPSYGVASVLAML 69
Db 141 VLGDALV-----DFSLKLYHAFSAKKKVTNMAFSPFSIASLLTQV 181

Qy 70 QLTGGETQQOIQAMGF-KIDKGMAPALRHLKELMGPWKDEISTTDAIFVQORDKLIV 129
Db 182 LLGAGENTKTNLEISLSPKFTCVHQALK-----GFTTKGVTVSQIFHSPDLAIR 233

Qy 130 QGFMHPFLFRSTVKQDFSEVERARFIINDVKTHTKGMISNLGKGAVDQLTRLVLV 189
Db 234 DTFV-NASRTLYSSPRVLSNNSDANLELINTVAKNTNNKISRLDLSLPSD--TRLVLL 290

Qy 190 NALYENGOWKTPFPDSSTHRLFLHKSOGSTVSVPMAQTNKFNTFTTPDGHYD---- 245
Db 291 NAIYLSAKWKTTFDPKTRMEFPFHFN-SVTKVPM-----NSKKY-----PVAHFIDQTLK 341

Qy 246 ----ILELPYHGDTLSMFIAAPYEKEVPLSALTNLISAQLISHWKGNNTRL-----PRL 295
Db 342 AKVQQLQSHN---LSIVILVQNLKXRLDEWEQALSP---SVFKAINELKMSKFQPTL 395

Qy 296 LVLPKFSLETEVDLRKPLENLGMDTFRQFQADFTSLSDQBPPLHVAQALQVKIEVNESG 355
Db 396 LTLPRIKVTTSDQMLSIKLEFFDF--SYDLNLCLGLTEPDLQVSAHQHQTVLELTETG 453

Qy 356 TVASSSTAVIVSARMAPEEIMDRPFLFVVRHNPTGTVLFMGQMEP 402
Db 454 VENAASAIISVARTLLVFEV--QQPFLPMLWDQKHKFFVFMGRVYDP 498

RESULT 12
US-11-186-284-187
; Sequence 187, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
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; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-187

Query Match      14.9%; Score 308.5; DB 7; Length 418;
Best Local Similarity 24.1%; Pred. No. 1.7e-20;
Matches 98; Conservative 80; Mismatches 212; Indels 17; Gaps 8;

Qy 3 MSPALTCLVLGLALVFGEGSAVHHPP--SYVAHLASDFGVRFQOQAQASKDRNVVPSY 60
Db 13 LEAALAAEVKPAAPGTAELKSPKATLAERSAGLAFSLYQAMAKDAQVENILVSPV 72

Qy 61 GVASVLAMLQLTGGETQQOIQAMGF-KIDDKGMAPALRHLKELMGPWKDEISTT-- 117
Db 73 VWASSGLVSLGGKATTASQAKAVLSAEQRDSEVHAGLGELLSLS---NSTARNVTWK 129

Qy 118 --DAIFVQRDLKLVQGFMPHFRLFRSTVKQDFSEVERARFIINDVKTHTKGMISNLL 175
Db 130 LGSRLYSPSSVPADDFVRSSKQHYNCEHSKINFRDKRRPLQSLNEWAAQTDDKLPVET 189

Qy 176 GKAVDQLTRLVLNLYFNGQWKTPFPDSSTHRLFLHKSOGSTVSVPMAQTNKFNYTE 235
Db 190 KD--VERTDALLVNAFFKPHDEKPHHQRVDNRGFMVTRSTYGVMMHRTGLYNYD 247

Qy 236 FTTPDGHYDILELPYHGDTLSMFIAAPYEKEVPLSALTNLISAQLISHWKGNNTRL 295
Db 248 ---DEKEKLQIVEMPLAHKLSSLIILMPHVE-PLERLEKLTKEQLKIWMGKMKKAVA 303

Qy 296 LVLPKFSLETEVDLRKPLENLGMDTFRQFQADFTSLSDQBPPLHVAQALQVKIEVNESG 355
Db 304 ISLPKGVVEVTHDLQKHLAGLGLTEADKDKADLSRMGSKKDLVLSVPHATAFELDTG 363

Qy 356 TVASSSTAVIVSARMAPEEIMDRPFLFVVRHNPTGTVLFMGQMEP 402
Db 364 NPFDQDIYGREELR-SPKLFYADHPFIFLVRDTQSGSLFLFGLRVRP 409

RESULT 13
US-10-821-234-1331
; Sequence 1331, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1331
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1331

Query Match      14.7%; Score 305; DB 6; Length 418;
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Best Local Similarity 23.7%, Pred. No. 3.4e-20;
Matches 94; Conservative 87; Mismatches 189; Indels 26; Gaps 10;

QY      15 ALVFGEGSAVHPPEPSYVAHLASDFGVVFQOQAASKDRNVVFSFYGVASVLAMLQLTTG 74
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      38 ALVEEDPPFKVPVNKLAADVSNFGYDLRVRSSTPTTNVLLSPLSVATALSLSLGA 97
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY      75 GETQQIQAAAMGFKIDDKGMAPALRHLYKELMGPMN--KDEISTDDAIFVQRDLKLVOGF 132
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      98 QRTESIHRALYY--DLISSPDIGHYKELLDTVTAPQKNLKASRIVFEKKLRIKSSF 154
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY      133 MPHFRLFRSTVK-----QVDFSEVERARPIINDWKTHTKGMISNLLGHGAVDQLTRL 186
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      155 VAPLEKSYGTRPRVLTGNPRLDQE-----INNVAQMKGKLARST-KEIPDETS-I 205
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY      187 VLNAVLYENGOWKTFFPDSSTRHRLFHKSOGSTVSVPMAQTAKNFNYTEFTTPDGHYVDI 246
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      206 LLLGVAHFQGQWVTKFSRKTSLSDFDYLDEBTRVRVPMMSDPKA--VURYGLSDLSCKI 263
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY      247 LELPYHGDTLISMFTAABEVEKPLSALTNILSAOLISHWGNMTRLPRLLVLPKFSLETE 306
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      264 AQLPLTG-SMSIIFFLPKVTQNLTIEESLTSFIHDI DRELXTVQAVLTVPKLKLSYE 322
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY      307 VDLRKPLENLGMTDMFRQFQADFTSLSDQEPFLHAQAALQKVYKIVNESGTVASSTAVIV 366
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      323 GEVTKSQEMKQLSLED--SPDFSKITG-KPIKLTOVEHRAGFEWNEDGAGTTPSGPQLP 379
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY      367 SARMAPBEITMDRPFLFVVRHNPTGTUVLFMGQVMPE 402
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      380 AHLTFPLDYHLNQPFIFVLVRTDTGALLFIGILDP 415
       :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||


RESULT 14
US-11-077-716-2
; Sequence 2, Application US/11077716
; Publication No. US20050260180A1
; GENERAL INFORMATION:
; APPLICANT: WEI, LISA
; APPLICANT: RASMUSSEN, HENRIK S
; TITLE OF INVENTION: MATERIALS AND METHODS FOR TREATING VASCULAR LEAKAGE IN T
; FILE REFERENCE: 233988
; CURRENT APPLICATION NUMBER: US/11/077,716
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,768
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-716-2
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247 LELPYGDTLSMFIAPAYEKEVPLSALTNTLSAQLSHWKGNNTRLPRLLVLPKFSLETE 306
264 AOLPLTG-SMSIIFFLPLKVQNTLTIIEESLTSEFHIDRELKTVOALVLPKLSYE 322
307 VDLRKPLENLGMDTMRFOQADFTSLSDQEPFLHVAQALQKVKIENESGTVASSSTAVIV 366
323 GEVTKSLOEWKLOSLED-SPDESKITG-KPIKLTQVEHRAGFEMNEDGAGTTTSPGLQP 379
367 SARMAPEEIIIMRPFLLFVVRHNPTGTVLFWGVNMP 402
380 AHLTFPLDYHLNQPFIFVLRLDTDTGALLFIGKILDP 415

RESULT 15
US-11-010-874-18
; Sequence 18, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-King
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND FIBROSIS
; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820.656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 18
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-010-874-18

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Search completed: December 13, 2005, 09:26:58
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2005, 09:01:30 ; Search time 39 Seconds
(without alignments)
991.773 Million cell updates/sec

Title: US-10-506-406-2
Perfect score: 2071
Sequence: 1 MQMSPALTCVLGLALVGE.....FVVRHNPVTGVLFGQVMEP 402

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	402	1	ITHUP1
2	1784	86.1	402	1	S05745
3	1746	84.3	400	2	JC4265
4	1680	81.1	402	1	A35032
5	1626	78.5	402	1	A34761
6	796.5	38.5	397	2	I48717
7	791.5	38.2	397	2	B27496
8	761	36.7	398	2	A37274
9	620	29.9	410	2	S70647
10	503.5	24.3	378	2	S38962
11	498.5	24.1	416	2	B23131
12	498	24.0	379	2	A42421
13	490	23.7	413	2	JX0267
14	487.5	23.5	418	2	S23675
15	486	23.5	413	2	JX0154
16	483.5	23.3	390	2	I38202
17	480	23.2	411	1	ITRT
18	480	23.2	413	2	S54981
19	479	23.1	379	2	S27383
20	479	23.1	403	2	S08102
21	476	23.0	413	2	I49473
22	474.5	22.9	464	1	XHHU3
23	472	22.8	413	2	I49472
24	470.5	22.7	465	2	I59611
25	469	22.6	415	2	A32853
26	468.5	22.6	408	2	A55533
27	468	22.6	376	1	A48681
28	468	22.6	413	2	I49470
29	467.5	22.6	374	2	A52773

ALIGNMENTS

RESULT 1

ITHUP1

plasminogen activator inhibitor 1 precursor [validated] - human
N:Alternate names: plasminogen activator inhibitor, endothelial

C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 05-Oct-2004
C:Accession: A28107; S02551; A26996; I59126; J50397; A25633; A26146; A29100; A25895; A25
R:Bosma, P.J.; van den Berg, E.A.; Kooistra, T.; Stenienlak, D.R.; Slightom, J.L.

J. Biol. Chem. 263, 9129-9141, 1988

A:Title: Human plasminogen activator inhibitor-1 gene. Promoter and structural gene nucl

A:Reference number: A28107; MUID:88243790; PMID:3132455

A:Accession: A28107

A:Molecule type: DNA

A:Residues: 1-402 <BOS>

A:Cross-references: UNIPROT:P05121; UNIPARC:UPI00000000CAB; GB:J03764; NID:g189564; PIDN:

R:Strandberg, L.; Lawrence, D.; NY, T.

Eur. J. Biochem. 176, 609-616, 1988

A:Title: The organization of the human plasminogen-activator-inhibitor-1 gene. Implicati

A:Reference number: S02551; MUID:89005111; PMID:3262512

A:Accession: S02551

A:Molecule type: DNA

A:Residues: 1-14, 'T', '16-402 <STR>

A:Cross-references: UNIPARC:UPI00001731AA; EMBL:X13338; NID:g35244; PIDN:CAA31722.1; PID

A:Note: the complete translation is not annotated in GenBank entries HSPA111, HSPA112, H

R:Loskutov, D.J.; Linders, M.; Keijer, J.; Veerman, H.; van Heerikhuizen, H.; Pannekoek

Biochemistry 26, 3763-3768, 1987

A:Title: Structure of the human plasminogen activator inhibitor 1 gene: nonrandom distri

A:Reference number: A26996; MUID:88000586; PMID:2820474

A:Accession: A26996

A:Molecule type: DNA

A:Residues: 1-402 <LOS>

A:Cross-references: UNIPARC:UPI00000000CAB; GB:M22321; GB:M17121; NID:g189576; PIDN:AAA60

A:Note: the sequence in GenBank entry HUMPA1B2, release 109.0, (PID:g189578) has the cod

R:van Zonneveld, A.J.; U.S.A. 85, 5525-5529, 1988

Proc. Natl. Acad. Sci.

A:Title: Type 1 plasminogen activator inhibitor gene: functional analysis and glucocorti

A:Reference number: I59126; MUID:88289754; PMID:2840665

A:Accession: I59126

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-9 <ZON>

A:Cross-references: UNIPARC:UPI000000038D; GB:J03836; NID:g189579; PIDN:AAA60010.1; PID

R:Follo, M.; Ginsburg, D.

Gene 84, 447-453, 1989

A:Title: Structure and expression of the human gene encoding plasminogen activator inh

A:Reference number: J50397; MUID:90128289; PMID:2612914

A:Accession: J50397

A:Molecule type: DNA

A:Residues: 85-86; 88-93; 166-171; 231-236; 298-302; 331-336; 360-365; 388-393 <FOL>

A:Cross-references: UNIPARC:UPI000011EC8E; UNIPARC:UPI000001731AB; UNIPARC:UPI000001731AC

1B1; GB:M33136; NID:g189543

A:Note: sequences of the intron/exon boundaries are shown

equamous cell carc
plasminogen activa
serine proteinase
alpha-1-antichymot
contrapsin precurs
antithrombin III -
alpha-1-antitrypsi
probable proteinase
MAP1 protein - myx
alpha-1 proteinase
plasminogen activa
hypothetical prote
alpha-1-antitrypsi
antithrombin III p
thyroxine-binding
serine proteinase

30 466.5 22.5 390 2 I38201
31 465.5 22.5 416 2 S19896
32 465 22.5 418 1 S31507
33 459 22.2 418 2 JH0494
34 458.5 22.1 418 2 JX0129
35 458.5 22.1 431 1 JX0364
36 458 22.1 413 2 A54968
37 455 22.0 361 2 A24470
38 455 22.0 369 2 B36418
39 455 22.0 413 2 I49474
40 455 22.0 415 2 S20047
41 454 21.9 374 2 AH1903
42 453.5 21.9 416 2 S21097
43 453.5 21.9 465 1 S28219
44 452.5 21.8 418 2 A39567
45 451.5 21.8 408 2 S11320

R;Pannekoek, H.; Veerman, H.; Lambers, H.; Diergaarde, P.; Verweij, C.L.; van Zonneveld, EMBO J. 5, 2539-2544, 1986
A;Title: Endothelial plasminogen activator inhibitor (PAI): a new member of the serpin g
A;Reference number: A91052; MUID:87053819; PMID:2430793
A;Accession: A25693
A;Molecule type: mRNA
A;Residues: 1-402 <PA>
A;Cross-references: UNIPARC:UPI00000000CAB; GB:X04429; NID:g35271; PIDN:CAA28025.1; PID:g
R;Ginsburg, D.; Zehnb, R.; Yang, A.Y.; Rafferty, U.M.; Andreasen, P.A.; Nielsen, L.; Dan
J. Clin. Invest. 78, 1673-1680, 1986
A;Title: cDNA cloning of human plasminogen activator-inhibitor from endothelial cells.
A;Reference number: A92766; MUID:87058123; PMID:3097076
A;Accession: A26146
A;Molecule type: mRNA
A;Residues: 1-402 <GN>
A;Cross-references: UNIPARC:UPI00000000CAB; GB:M16006; NID:g189541; PIDN:AAA60003.1; PID:
R;Wun, T.C.; Kretzmer, K.K.
FEBS Lett. 210, 11-16, 1987
A;Title: cDNA cloning and expression in E. coli of a plasminogen activator inhibitor (PA
A;Reference number: A29100; MUID:87105925; PMID:3026837
A;Accession: A29100
A;Molecule type: mRNA
A;Residues: 17-402 <N>
A;Cross-references: UNIPARC:UPI000016AE5E; GB:X04744; NID:g35275; PIDN:CAA28444.1; PID:g
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Ny, T.; Sawdey, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 6776-6780, 1986
A;Title: Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-
A;Reference number: A25895; MUID:86313660; PMID:3092219
A;Accession: A25895
A;Molecule type: mRNA
A;Residues: 20-402 <NYT>
A;Cross-references: UNIPARC:UPI00001423AD; GB:M14083; NID:g189566; PIDN:AAA60008.1; PID:
R;Andreasen, P.A.; Riccio, A.; Welinder, K.G.; Douglas, R.; Sartorio, R.; Nielsen, L.S.;
FEBS Lett. 209, 213-218, 1986
A;Title: Plasminogen activator inhibitor type-1: reactive center and amino-terminal hete
A;Reference number: A91371; MUID:87080762; PMID:3025016
A;Accession: A25651
A;Molecule type: mRNA
A;Residues: 1-14, "16-47 <AND1>
A;Cross-references: UNIPARC:UPI000016AE5C; GB:X04729; NID:g35263; PIDN:CAA28438.1; PID:g
A;Accession: B25651
A;Molecule type: mRNA
A;Residues: 364-402 <AND2>
A;Cross-references: UNIPARC:UPI000016AE5B; GB:X04731; NID:g35260; PIDN:CAA28442.1; PID:g
R;Laug, W.E.; Abersold, R.; Jong, A.; Rideout, W.; Bergman, B.L.; Baker, J.
Thromb. Haemost. 61, 517-521, 1989
A;Title: Isolation of multiple types of plasminogen activator inhibitors from vascular s
A;Reference number: A60436; MUID:90020174; PMID:2799763
A;Accession: A60436
A;Molecule type: protein
A;Residues: 225-235 <LAU>
A;Cross-references: UNIPARC:UPI00001731B2
R;Kjoller, L.; Martensen, P.M.; Sottrup-Jensen, L.; Justesen, J.; Rodenburg, K.W.; Andre
Eur. J. Biochem. 241, 38-46, 1996
A;Title: Conformational changes of the reactive-centre loop and beta-strand 5A accompany
A;Reference number: S74133; MUID:97054589; PMID:8898886
A;Accession: S74133
A;Molecule type: protein
A;Residues: 22-30,370-376 <KJO>
A;Cross-references: UNIPARC:UPI00001731B3; UNIPARC:UPI000001731B4
R;Sroenqvist, M.; Karlsson, K.E.; Bjoerquist, P.; Andersson, J.O.; Bystroem, M.; Hanssc
Biochim. Biophys. Acta 1295, 103-109, 1996
A;Title: Characterization of the complex of plasminogen activator inhibitor type 1 with
A;Reference number: S70346; MUID:96283799; PMID:8679667
A;Accession: S70346
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 370-375 <STO>
A;Cross-references: UNIPARC:UPI00001731B5
C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:UKHUT
fibrinolysis. High concentrations of this protein have been associated with human throm
, C;Comment: Three types of PAI have been identified (see also PIR:A32853 and PIR:A39339)

oma cells. Vascular endothelial cells may be the primary site of synthesis of plasma PAI
C;Comment: Glycosylation is not required for inhibitory activity.

C;Genetics:
A;Gene: GDB:PA11; PLANHI
A;Cross-references: GDB:120297; OMIM:173360
A;Map position: 7q21.3-7q22
A;Introns: 91/1, 169/1, 234/1, 300/2, 334/1, 363/1, 391/1
C;Superfamily: serpin
C;Keywords: glycoprotein; serine proteinase inhibitor
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-402/Product: plasminogen activator inhibitor-1 #status experimental <MAT>
F;232-288.352/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;369/Inhibitory site: Arg (plasminogen activator) #status predicted

Query Match 100.0%; Score 2071; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.5e-155;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQMSPALTCVLGLALVFGEGSAVHHPPSSVAHLASDFGVRVFOQVAQASKDRNVVFSFY	60
Db	1	MQMSPALTCVLGLALVFGEGSAVHHPPSSVAHLASDFGVRVFOQVAQASKDRNVVFSFY	60
Qy	61	GVASVLAMQLQTTGGSTQQOIQAAAGFKIDDKMAPALRHLHYKELMGPNKDEISTTDAI	120
Db	61	GVASVLAMQLQTTGGSTQQOIQAAAGFKIDDKMAPALRHLHYKELMGPNKDEISTTDAI	120
Qy	121	FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARPIINDWVKTHTKGMISNLLKGAV	180
Db	121	FVQRDLKLVQGFMPHFRLFRSTVKQVDFSEVERARPIINDWVKTHTKGMISNLLKGAV	180
Qy	181	DOLTRVLVNLALYFNGOWKTPPDSSTHRRLFHKSOGSTVSPVMAQTNNKFNYTEFTTPD	240
Db	181	DQLTRVLVNLALYFNGOWKTPPDSSTHRRLFHKSOGSTVSPVMAQTNNKFNYTEFTTPD	240
Qy	241	GHYVDILELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHKGNMTLRLLVLPK	300
Db	241	GHYVDILELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHKGNMTLRLLVLPK	300
Qy	301	FSLETEVDLRKPLENLGMDTDFRQFQADFTSLSDQPLHVAQALQKVIENESGTVASS	360
Db	301	FSLETEVDLRKPLENLGMDTDFRQFQADFTSLSDQPLHVAQALQKVIENESGTVASS	360
Qy	361	STAVIVSARMAPEEIIIMDRPFLFVVRHNPVTGTVLFMGQWMEP	402
Db	361	STAVIVSARMAPEEIIIMDRPFLFVVRHNPVTGTVLFMGQWMEP	402

RESULT 2

S06745
plasminogen activator inhibitor-1 precursor - bovine
N;Alternate names: endothelial-cell plasminogen activator inhibitor; PAI-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1990 #sequence revision 22-Apr-1995 #text_change 05-Oct-2004
C;Accession: S06745; A35855; S01324; S10906
R;Mimuro, J.; Sawdey, M.; Hattori, M.; Luskutoff, D.J.
Nucleic Acids Res. 17, 887, 1989
A;Title: cDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).
A;Reference number: S06745; MUID:90067867; PMID:2587231
A;Accession: S06745
A;Molecule type: mRNA
A;Residues: 1-402 <NIM>
A;Cross-references: UNIPROT:P1309; UNIPARC:UPI000002PEA6; EMBL:X16383; NID:g560; PIDN:G
R;Pepper, M.S.; Beiln, D.; Montesano, R.; Orci, L.; Vassalli, J.D.
J. Cell Biol. 111, 743-755, 1990
A;Title: Transforming growth factor-beta 1 modulates basic fibroblast growth factor-induc
A;Reference number: A35855; MUID:90338128; PMID:1696269
A;Accession: A35855
A;Molecule type: mRNA
A;Residues: 153-235 <PEP>
A;Cross-references: UNIPARC:UPI000016C357; EMBL:X52906; NID:g598; PIDN:CAA37094.1; PID:g
R;Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.
Eur. J. Biochem. 176, 81-87, 1988
A;Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and heat

A:Reference number: S01324; MUID:88329072; PMID:3262060
A:Accession: S01324
A:Molecule type: protein
A:Residues: 24-49, 'L', 51-63 <KAT>
A:Cross-references: UNIPARC:UPI00001731B8
C:Comment: Three types of PAI have been identified. PAI-1 is an acid-stable glycoprotein
may be the primary site of synthesis of plasma PAI.
C:Comment: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, and
ysis.
C:Comment: Glycosylation is not a prerequisite for inhibitory activity.
C:Superfamily: serpin
C:Keywords: glycoprotein; serine proteinase inhibitor
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-402/Product: plasminogen activator inhibitor 1 #status predicted <MAT>
F:232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:369/Inhibitory site: Arg (plasminogen activator) #status predicted

Query Match 86.1%; Score 1784; DB 1; Length 402;
Best Local Similarity 85.3%; Pred. No. 9,8e-133;
Matches 343; Conservative 29; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MQMSPALCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
Db 1 MEMSPVACLALGLALIFEGGSAYQPOSAASLATDFGVKVFQVVRASKDRNVVFSY 60

Qy 61 GVASVLAMQLTGTGETQQOIQAMGPKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVASVLAMQLTGTGETQQOIQAMGPKIEEGGNAPAFHRLYKELMGPNKDEISTADAI 120

Qy 121 FVQRDLKLVQGMFHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180
Db 121 FVQRDLKLVQGMFHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180

Qy 181 DQTLRLVLNVALYFNGQWKTPPPDSSTHRLFHKSDGSTSVSPMMAQTNKFNTEFTTPD 240
Db 181 DQTLRLVLNVALYFNGQWKMPPESTHRLFHKSDGSTISVPMMAQTNKFNTEFTTPD 240

Qy 241 GHYDILELPHGDTLSMFIAPYKEVPLSALTNILSAQLISHKGNMTRLPRLLLVLPK 300
Db 241 GRYYDILELPHGNTLSMFIAPYKEVPLSALTSLDAELISQKGNMTRLRLLVLPK 300

Qy 301 FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQELPHVAQALQKVKIEVNESGTVA 360
Db 301 FSLETEIDRRPLENLGTMDFRPPQADFFSSDQELFVLSQALQKVKIEVNESGT 360

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 361 STALIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

RESULT 3
JC4265
plasminogen activator inhibitor type 1 precursor - American mink
C:Species: Mustela vison (American mink)
C:Date: 19-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
C:Accession: JC4265
R:Chuang, T.H.; Hamilton, R.T.; Nilsen-Hamilton, M.
Gene 162, 303-308, 1995
A:Title: Cloning of the mink plasminogen activator inhibitor type-1 messenger RNA: An m
A:Reference number: JC4265; MUID:96032362; PMID:7557448
A:Accession: JC4265
A:Molecule type: mRNA
A:Residues: 1-400 <CHU>
A:Cross-references: UNIPROT:P50449; UNIPARC:UPI0000131217; EMBL:X58541; NID:g1164923; PI
A:Experimental source: lung CCL64 epithelial cells
C:Comment: This protein controls the activities of the plasminogen activators and plasmi
C:Genetics:
A:Gene: pai-1
C:Superfamily: serpin
C:Keywords: glycoprotein; plasminogen activator; serine proteinase inhibitor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-400/Product: plasminogen activator inhibitor type 1 #status predicted <MAT>
F:230,286,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:367/Inhibitory site: Arg (plasminogen activator) #status predicted

Query Match 84.3%; Score 1746; DB 2; Length 400;
Best Local Similarity 85.3%; Pred. No. 9,6e-130;
Matches 343; Conservative 25; Mismatches 32; Indels 2; Gaps 1;

Qy 1 MQMSPALCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFOQVAQAKDRNVVFSY 60
Db 1 MQMS--TVCLALGLALVFGEGSASLYHETRAAELATDFGVKVFQVAQAKDRNVVFSY 58

Qy 61 GVASVLAMQLTGTGETQQOIQAMGPKIDDKGNAPALRHLYKELMGPNKDEISTTDAI 120
Db 59 GLASVLAMQLTGTAGETQQOIQEAMRFQIDKGNAPALRQLYKELMGPNKDEISTADAI 118

Qy 121 FVQRDLKLVQGMFHFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKAV 180
Db 119 FVQRDLKLVHGMFHFRLFQTTVKQVDFSEVERARFIINDWVKRHTKGMIGDILGRGT 178

Qy 181 DQTLRLVLNVALYFNGQWKTPPPDSSTHRLFHKSDGSTSVSPMMAQTNKFNTEFTTPD 240
Db 179 DQTLRLVLNVALYFNGQWKTPFPKSGTHRLFHKSDGSTVSPMMAQTNKFNTEFTSTPE 238

Qy 241 GHYDILELPHGDTLSMFIAPYKEVPLSALTNILSAQLISHKGNMTRLPRLLLVLPK 300
Db 239 GRYYDILELPHGDTLSMFIAPYKEVPLSALTNLDAQLISQKGNMTRLRLLVLPK 298

Qy 301 FSLETEVDLRKPLENLGTMDFROFQADFTSLSDQELPHVAQALQKVKIEVNESGTVA 360
Db 299 FSLESEVNLRLPLENLGTMDFRNQADFFSSLSQELALYVSQALQKVKIEVNESGTVA 358

Qy 361 STAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
Db 359 STALIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFMGQVMEP 400

RESULT 4
A35032
plasminogen activator inhibitor 1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: A35032; A60581; A39120
R:Brudzinski, C.J.; Riordan-Johnson, M.; Nordby, E.C.; Suter, S.M.; Gelehrter, T.D.
J. Biol. Chem. 265, 2078-2085, 1990
A:Title: Isolation and characterization of the rat plasminogen activator inhibitor-1 gen
A:Reference number: A35032; MUID:90130456; PMID:2298740
A:Accession: A35032
A:Molecule type: DNA
A:Residues: 1-402 <BRU>
A:Cross-references: UNIPROT:P20961; UNIPARC:UPI0000131219; GB:J05206; NID:g205965; PIDN
R:Zeheb, R.; Gelehrter, T.D.
Gene 73, 459-468, 1988
A:Title: Cloning and sequencing of cDNA for the rat plasminogen activator inhibitor-1.
A:Reference number: JT0490; MUID:89211983; PMID:3149611
A:Accession: JT0490
A:Molecule type: mRNA
A:Residues: 1-402 <ZEH>
A:Cross-references: UNIPARC:UPI0000131219; GB:M24067; NID:g577500; PIDN:AAA56856.1; PID
R:Newman, M.J.; Lane, E.A.; Iannotti, A.M.; Nugent, M.A.; Pepinsky, R.B.; Keeki-Oja, J.
Endocrinology 126, 2936-2946, 1990
A:Title: Characterization and purification of a secreted plasminogen activator inhibitor.
on in transformed NRK cells.
A:Reference number: A60581; MUID:90276328; PMID:2190800
A:Accession: A60581
A:Molecule type: protein
A:Residues: 24-48 <NEW>
A:Cross-references: UNIPARC:UPI00001731B6
R:Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhli, W.C.; Raizada, M.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991
A:Title: Angiotensin II induces secretion of plasminogen activator inhibitor 1 and a tti
A:Reference number: A39120; MUID:91156719; PMID:2000398
A:Accession: A39120
A:Status: preliminary
A:Molecule type: protein

A;Residues: 24-43,'G' <OLS>
A;Cross-references: UNIPARC:UPI00001731B7
C;Genetics:
A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1; 363/1; 391/1
C;Superfamily: serpin
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-402/Product: plasminogen activator inhibitor-1 #status experimental <MAT>
F;8,232,352/Binding site: carboxylate (Asn) (covalent) #status predicted
F;369/Inhibitory site: Arg (plasminogen activator) #status predicted

Query Match 81.1%; Score 1680; DB 1; Length 402;
Best Local Similarity 80.8%; Pred. No. 1.5e-124;
Matches 325; Conservative 36; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFEGESAVHHPPSYVAHLLASDFGVRVFOQVAQAKDRNVVFSY 60
Db 1 MQMSSALTCLTLGLVLVFGKGFASPLPESHQAQATNFGVKVFQHVQVQAKDRNVVFSY 60

Qy 61 GVASVLAMLQLTGGETTQOOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVSSVLAMLQLTGAGTRQOIQDAMGFKNVEKGTAAHALRQLSKELMGPNKNEISTADAI 120

Qy 121 FVQRDLKLVOGFMFPHFRPRSTVKQVDFSEVERARFIINDWVTKTKGMSNLLGKAV 180
Db 121 FVQRDLKLVOGFMFPHFRPRSTVKQVDFSEVERARFIINDWVTKTKGMSNLLGKAV 180

Qy 181 DQLTRVLVNLALVFNGQWKTFFPDSTHRRFLFKSDGSTSVSPMAQTNKFNTEFTTPD 240
Db 181 NELTRVLVNLALVFNGQWKTFFLEASTHQRLFKHSDGSTISVPMQAQNNKFNTEFTTPD 240

Qy 241 GHYDIILELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLLLVLPK 300
Db 241 GHEYDIILELPYHGDTLSMFIAPAEKDVPLSAITNILDALIRQWKNMTRPLRLLILPK 300

Qy 301 FSLTEVDLRKPLENLGMDMFRQFADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Db 301 FSLTEVDLRKPLENLGMDTIFSSQTADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360

Qy 361 STAVIVSARMAPEIIMDRPFLFVRHNPTGTVLFMQGVMEP 402
Db 361 STALLVSARMAPEIIMDRPFLFVRHNPTGTVLFMQGVMEP 402

RESULT 5
A34761
plasminogen activator inhibitor 1 homolog mr1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A34761; S48208
R;Prendergast, G.C.; Diamond, L.E.; Dahl, D.; Cole, M.D.
Mol. Cell. Biol. 10, 1265-1269, 1990
A;Title: The c-myc-regulated gene mr1 encodes plasminogen activator inhibitor 1.
A;Reference number: A34761; MUID:90158593; PMID:2406566
A;Accession: A34761
A;Molecule type: mRNA
A;Residues: 1-402 <PRE>
A;Cross-references: UNIPROT:P22777; UNIPARC:UPI00000298B9; GB:M33960; NID:g200219; PIDN:
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48208
A;Molecule type: protein
A;Residues: 'M',24-29 <LIJ>
A;Cross-references: UNIPARC:UPI00001731B9
C;Superfamily: serpin

Query Match 78.5%; Score 1626; DB 1; Length 402;
Best Local Similarity 78.6%; Pred. No. 2.7e-120;
Matches 316; Conservative 41; Mismatches 45; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLGLALVFEGESAVHHPPSYVAHLLASDFGVRVFOQVAQAKDRNVVFSY 60

Db 1 MQMSSALACLILGLVLVSGKFTLPLRESHTAQADTFGVKVFQVVQASKDRNVVFSY 60
Qy 61 GVASVLAMLQLTGGETTQOOIQAAAGFKIDDKGMAPALRHLYKELMGPNKDEISTTDAI 120
Db 61 GVSSVLAMLQMTTAGTRRQIQDAMGFKNVEKGTAAHALRQLSKELMGPNKNEISTADAI 120

Qy 121 FVQRDLKLVOGFMFPHFRPRSTVKQVDFSEVERARFIINDWVTKTKGMSNLLGKAV 180
Db 121 FVQRDLKLVOGFMFPHFRPRSTVKQVDFSEVERARFIINDWVTKTKGMSNLLGKAV 180

Qy 181 DQLTRVLVNLALVFNGQWKTFFPDSTHRRFLFKSDGSTSVSPMAQTNKFNTEFTTPD 240
Db 181 DEUTRLVLVNLALVFSGQWKTFFLEASTHQRLFKHSDGSTSVSPMAQSNKFNTEFTTPD 240

Qy 241 GHYDIILELPYHGDTLSMFIAPAEYKEVPLSALTNILSAQLISHWKGNTMLRPLLLVLPK 300
Db 241 GLEYDVVELPYQDRDLSMFIAPAEKDVPLSALTNLIDALIRQWKNMTRPLRLLILPK 300

Qy 301 FSLTEVDLRKPLENLGMDMFRQFADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360
Db 301 FSLTEVDLRKPLEKLMFMPDSATLADFTSLSDQEPHLVAQALQKVKIEVNESGTVASS 360

Qy 361 STAVIVSARMAPEIIMDRPFLFVRHNPTGTVLFMQGVMEP 402
Db 361 STAFVISARMAPEIIMDRPFLFVRHNPTGTVLFMQGVMEP 402

RESULT 6
I48717
protease inhibitor nexin I precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I48717; S70772; S35731
R;Vassalli, J.D.; Huarte, J.; Bosco, D.; Sappino, A.P.; Velardi, A.; Wohlweil,
EMBO J. 12, 1871-1878, 1993
A;Title: Protease-nexin I as an androgen-dependent secretory product of the murine semin
A;Reference number: I48717; MUID:93259128; PMID:8491179
A;Accession: I48717
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-397 <RES>
A;Cross-references: UNIPROT:Q07235; UNIPARC:UPI000004078; EMBL:X70296; NID:9551064; PID:
A;Accession: S70772
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-86 <VAS>
A;Cross-references: UNIPARC:UPI000016CFB8; EMBL:X70946; NID:957930; PIDN:CAA50285.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1993
C;Genetics:
A;Gene: PN-1
C;Superfamily: serpin
C;Keywords: serine proteinase inhibitor
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-397/Product: proteinase inhibitor nexin I #status predicted <MAT>

Query Match 38.5%; Score 796.5; DB 2; Length 397;
Best Local Similarity 43.0%; Pred. No. 5.5e-55;
Matches 159; Conservative 74; Mismatches 134; Indels 3; Gaps 2;

Qy 34 LASDFGVRVFOQVAQAKDRNVVFSYGVASVLAMLQLTGGETTQOOIQAAAGFKIDDKG 93
Db 30 LGSNTGIGVFNQITIKSRPHENVVVSPHGIASILGMLQLGADGKTKKQLSTVMRYNVN--G 87

Qy 94 MAPALRHLYKELMGPNKDEISTTDAIFVQRDLKLVOGFMFPHFRPRSTVKQVDFSEVE 153
Db 88 VGKVLKKINKAIIVSKKQKDIIVTAVNAVFLNFGFMEVPEFAVRKNDVFOCEVQNVNFDPA 147

Qy 154 RARFIINDWVTKTKGMSNLLGKAVD-QLTRVLVNLALVFNGQWKTTPPDSTHRRLF 212
Db 148 SASSEINFVWKNETRGMDNLNLSPLNLDGALTRVLVNLAVVYFKGLWKSRFOPESTKKRTF 207

Qy 213 HKSDGSTSVSPMAQTNKFNTEFTTPDGHYYDILFLPYHGDTLSMFIAPAEYKEVPLSA 272

Db 208 VAGDKSYQVPMQLAQSLVFRSGSTRTPNGLWYNFIELPYHGESISMLIALTESSTPLSA 267
 Qy 273 LTNILSAQLISHWKGNNMTRLLPRLVLPKFSLETEVDLRKPLENLGMDTMDRPFQFQADFTSL 332
 Db 268 IIPHTTTKIDSWMNTWPKRMQLVLPKFTAVAOQDLKEPLKALGITEMFEPFSKANFTKI 327
 Qy 333 SDQEPPLHVAQALQKVKIENVESGTVASSSTAVIVSARMAPBEIIMDRPFLFVVRHNPVTGT 392
 Db 328 TRSLSLHVSHLQAKIEVSDGTAKAAVTTAILIARSPFPWFIVDRPFLFCIRHNPTGA 387
 Qy 393 VLFGQVMEP 402
 Db 388 ILFLGQVKNP 397

RESULT 7

protease inhibitor nexin 1 precursor - rat (fragment)
 N:Alternate names: glia-derived nexin (GDN)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 05-Oct-2004
 C:Accession: B27496; A42351; B42351; C42351
 R:Sommer, J.; Gloor, S.M.; Rovelli, G.F.; Hofsteenge, J.; Nick, H.; Meier, R.; Monard, D.
 Biochemistry 26, 6407-6410, 1987
 A:Title: CDNA sequence coding for a rat glia-derived nexin and its homology to members of the superfamily: serpin
 A:Reference number: A90519; MUID:88107544; PMID:3427015
 A:Accession: B27496
 A:Molecule type: mRNA
 A:Residues: 1-397 <SOM>
 A:Cross-references: UNIPROT:P07092; UNIPARC:UPI000002BD9D; GB:M17784; NID:G204283; PIDN:G204283
 A:Note: The authors translated the codon TGG for residue 156 as Thr
 R:Nick, H.; Hofsteenge, J.; Shaw, E.; Rovelli, G.; Monard, D.
 Biochemistry 29, 2417-2421, 1990
 A:Title: Functional sites of glia-derived nexin (GDN): importance of the site reacting with the heparin-binding site of glia-derived nexin/protease nexin
 A:Reference number: A42351; MUID:90248459; PMID:2337608
 A:Accession: A34538
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 364-394 <NIC>
 A:Cross-references: UNIPARC:UPI000017631F
 R:Rovelli, G.; Stone, S.R.; Guidolin, A.; Sommer, J.; Monard, D.
 Biochemistry 31, 3542-3549, 1992
 A:Title: Characterization of the heparin-binding site of glia-derived nexin/protease nexin
 A:Reference number: A42351; MUID:92207980; PMID:1554734
 A:Accession: A42351
 A:Molecule type: protein
 A:Residues: 82-96 <ROVI>
 A:Cross-references: UNIPARC:UPI00000E761E
 A:Note: sequence extracted from NCBI backbone (NCBIP:93846)
 A:Accession: B42351
 A:Molecule type: protein
 A:Residues: 165-178 <ROV2>
 A:Cross-references: UNIPARC:UPI00000E5D4A
 A:Note: sequence extracted from NCBI backbone (NCBIP:93851)
 A:Accession: C42351
 A:Molecule type: protein
 A:Residues: 317-333 <ROV3>
 A:Cross-references: UNIPARC:UPI00000E5B74
 A:Note: sequence extracted from NCBI backbone (NCBIP:93856)
 A:Note: peptide sequences were determined from rat CDNA cloned and expressed in yeast
 C:Superfamily: serpin
 C:Keywords: glycoprotein; serine proteinase inhibitor
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-397/Product: proteinase inhibitor nexin 1 #status predicted <MAT>
 F:159/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 38.2%; Score 791.5; DB 2; Length 397;
 Best Local Similarity 42.7%; Pred. No. 1.4e-54;
 Matches 158; Conservative 72; Mismatches 137; Indels 3; Gaps 2;

Qy 34 LASDFGVRFQVQAQSKDRNVVFSYGVASVLAQLTGGTGTQQIQAAAGFKIDDKG 93

Db 30 LGSDTGIQVFNQIKSQPHENVVISHGIIASILGMLQGLADGRTKKQLSTVMRYNVN--G 87
 Qy 94 MAPALRLHYKELMCPNKNKDISITTDALFVORDLKLVOGFMHPFRLFRSTVQKQVDFSEVE 153
 Db 88 VGKVLKINKAIKVSCKNDIVTVNAVVRNGFKVEVFAARNKEVQCEVQSVNFQDPA 147
 Qy 154 RARFIINDWVKTHTKGMSNLLGKGAVDQ-LTRLVLNVALYFNGOWKTPPPDPSSTHRLRF 212
 Db 148 SACDAINFVQVETRGMDNLLSPNLDLSALTLLVLNAVYFKGLWKSRFQENTKKRTF 207
 Qy 213 HKSGDSTVSPMMAQTNKFNFTTDPGHYDILELPHYGDTLSMFTAAPYKEVEVPLSA 272
 Db 208 VAGDKSYQVPMQLAQSLVFRSGSTRTPNGLWYNFIELPYHGESISMLIALTESSTPLSA 267
 Qy 273 LTNILSAQLISHWKGNNMTRLLPRLVLPKFSLETEVDLRKPLENLGMDTMDRPFQFQADFTSL 332
 Db 268 IIPHTTTKIDSWMNTWPKRMQLVLPKFTAVAOQDLKEPLKALGITEMFEPFSKANFTKI 327
 Qy 333 SDQEPPLHVAQALQKVKIENVESGTVASSSTAVIVSARMAPBEIIMDRPFLFVVRHNPVTGT 392
 Db 328 TRSLSLHVSHLQAKIEVSDGTAKAAVTTAILIARSPFPWFIVDRPFLFCIRHNPTGA 387
 Qy 393 VLFGQVMEP 402
 Db 388 ILFLGQVKNP 397

RESULT 8

A37274
 glia-derived nexin I precursor, splice form beta - human
 N:Alternate names: glia-derived neurite promoting factor; proteinase inhibitor 7; protei
 N:Contains: glia-derived nexin I precursor, splice form alpha
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 05-Oct-2004
 C:Accession: A37274; J00010; A27496; A26061; A24051
 R:McGrogran, M.; Kennedy, J.; Li, M.P.; Hsu, C.; Scott, R.W.; Simonsen, C.C.; Baker, J.B.
 Bio/Technology 6, 172-177, 1988
 A:Title: Molecular cloning and expression of two forms of human protease nexin I.
 A:Reference number: J00010
 A:Accession: A37274
 A:Molecule type: mRNA
 A:Residues: 1-398 <MCG1>
 A:Cross-references: UNIPROT:P07093; UNIPARC:UPI00000049599
 A:Experimental source: splice form beta
 A:Accession: J00010
 A:Molecule type: mRNA
 A:Residues: 1-328, R', 331-398 <MCG2>
 A:Cross-references: UNIPARC:UPI00000009F3
 A:Experimental source: splice form alpha
 R:Sommer, J.; Gloor, S.M.; Rovelli, G.F.; Hofsteenge, J.; Nick, H.; Meier, R.; Monard, D.
 Biochemistry 26, 6407-6410, 1987
 A:Title: CDNA sequence coding for a rat glia-derived nexin and its homology to members of the superfamily: serpin
 A:Reference number: A90519; MUID:88107544; PMID:3427015
 A:Accession: A27496
 A:Molecule type: mRNA
 A:Residues: 1-328, R', 331-398 <SOM>
 A:Cross-references: UNIPARC:UPI000000D9F3; GB:M17783; NID:G183063; PIDN:AAA35883.1; PID
 R:Gloor, S.; Odink, K.; Guenther, J.; Nick, H.; Monard, D.
 Cell 47, 687-693, 1986
 A:Title: A glia-derived neurite promoting factor with protease inhibitory activity belo
 A:Reference number: A26061; MUID:87051740; PMID:287774
 A:Accession: A26061
 A:Molecule type: protein
 A:Residues: 1-259, S', 261-398 <GLO>
 A:Cross-references: UNIPARC:UPI000017631D
 R:Scott, R.W.; Bergman, B.L.; Bajpai, A.; Herish, R.T.; Rodriguez, H.; Jones, B.N.; Barr
 J. Biol. Chem. 260, 7029-7034, 1985
 A:Title: Protease nexin. Properties and a modified purification procedure.
 A:Reference number: A24051; MUID:85207723; PMID:3997857
 A:Accession: A24051
 A:Molecule type: protein
 A:Residues: 20-47 <SCO>
 A:Cross-references: UNIPARC:UPI000017631E

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